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#23102

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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In re Application of: Heard et al.

Title: DISEASE-INDUCED POLYNUCLEOTIDES

Serial No.: 09/533,029

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Examiner: Kruse, D.

Group Art Unit: 1638

Commissioner for Patents
Washington, D.C. 20231

DECLARATION UNDER 37 CFR 1.132 OF JACQUELINE E. HEARD

I, Jacqueline E. Heard, declare:

1. I received my doctoral degree from Boston College, Boston, Mass., in 1996. I have held the position of Senior Scientist at Mendel Biotechnology, Inc., Hayward, California, since March, 1998 and Director of the Genomics Program since January, 2002. In this declaration, I serve as an expert witness in that my work has involved the isolation and characterization of plant genes and the use of cloned genes to modify a variety of traits in genetically transformed plants, specifically in the areas of biotic and abiotic stress responses. I am also a named inventor of at least one of the non-selected sequences of the present application and I am therefore familiar with the instant invention.
2. This application relates to compositions and methods for modifying a plant's traits. The compositions include polynucleotides which encode novel plant transcription factor polypeptides first identified in *Arabidopsis thaliana*, a plant used experimentally as a model for all plant species. The methods include using the polynucleotides and polypeptides to modify a trait, such as a plant's response to environmental stress, in a transgenic plant.
3. I understand that the Examiner has rejected claims 17-36 directed to the described invention based on lack of enablement. The Examiner has stated that: 1) the specification does not provide reasonable enablement that a plant having the amino acid sequence of SEQ ID NO:18 can enhance the plant's tolerance to salt, heat, drought, osmotic stress, cold, freezing, or nutrient or pathogen stress 2) the specification does not provide reasonable enablement that a plant transformed with a polynucleotide encoding a polypeptide sequence of SEQ ID NO:18 can enhance the plant's tolerance to salt, heat, drought, osmotic stress, cold, freezing, or nutrient or pathogen stress, and 3) the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

4. I would like to address the Examiner's concerns as to the enablement of the claimed invention by the specification. Applicants disclosed particular polynucleotide sequences encoding plant transcription factor polypeptides that were induced when plants were exposed to either biotrophic or necrotropic plant pathogens, such as *Fusarium*, *Erysiphe*, and *Botrytis*; and disease associated growth-regulators such as methyl jasmonate (see specification at page 7, lines 22-27; page 8, lines 34-35; and page 19, lines 33-35). Applicants disclosed how to identify such induced polynucleotide sequences using RT-PCR and microarray experiments (see specification at page 19, lines 32-36; page 21, lines 10-28).

5. I herewith submit a set of four tables which report the results of such microarray analyses (Exhibits A-D). All these analyses were performed by one of the named inventors prior to the date of filing of the instant application. Exhibit A shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 3-fold at 24 hours following treatment of native plants with the plant pathogen *Fusarium* (see Exhibit A, page 2). Exhibit B shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2.3-fold at 48 hours following treatment of native plants with *Fusarium* (see Exhibit B, page 11). Exhibit C shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2-fold at 7 days following treatment of native plants with the plant pathogen *Erysiphe* (see Exhibit C, page 19). Exhibit D shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2-fold at 24 hours following treatment of native plants with methyl jasmonate (see Exhibit D, page 3). In support of these results, a set of subsequent experiments, reported in Exhibits E, , shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2.6-fold at 12 hours following treatment of native plants with the plant pathogen *Botrytis* (see Exhibit E, page 4); was upregulated by at least . Applicants therefore had disclosed in the specification that they were in possession of the invention at the time the application was filed.

6. Applicants disclosed in the specification that the polynucleotides and polypeptides of the invention may be used to modify plant development, physiology or biochemistry such that the modified plants have a trait advantage over wild type plants (see specification at page 9, lines 21-23; page 16, lines 10-17; page 17, lines 10-15; page 21, line 32 through page 25, line 4).

7. I herewith submit a report of such analyses which show that when G28 (SEQ ID NO:17 of the instant application) is overexpressed in a transgenic plant, the transgenic plant is more resistant to infection with *Erysiphe*, as Applicants had predicted and disclosed in the specification (see Exhibit H, under heading "Mendel Discoveries").

8. In addition to the microarray analysis results for G28 (SEQ ID NO:17) as presented above, I would like to submit that mRNA levels of SEQ ID NO:12 (G4; Exhibit A, page 7), SEQ ID NO:22 (G19; Exhibit F, page 2), SEQ ID NO:34 (G1006; Exhibit A, page 2; Exhibit C, page 9; Exhibit E, page 4;

Exhibit F, page 1), and SEQ ID NO:82 (G25; exhibit G, page 4) also were upregulated by at least about 2-fold by plant pathogens such as *Fusarium*, *Erysiphe*, and *Botrytis*; and by methyl jasmonate, as Applicants disclosed in the Specification. Therefore, it is my contention that Applicants had disclosed several polynucleotide species in the instant application which, when overexpressed in a transgenic plant, would endow the plant with increased pathogen resistance.

9. It is my contention that one of ordinary skill in the art would have reasonably believed that Applicants therefore had disclosed the invention at the time the application was filed.

10. The function of SEQ ID NOS:17 and 18 (G28) has been analyzed using transgenic *Arabidopsis* plants in which this gene was expressed under the control of a 35S promoter, as disclosed in the specification. *Arabidopsis* plant lines overexpressing SEQ ID NO:17 (G28) repeatedly showed in laboratory experiments to be more tolerant to infections by *Erysiphe orontii*, *Sclerotinia sclerotiorum*, or *Botrytis cinerea*. In a repeat experiment using individual lines, all plant lines analyzed showed improved tolerance to *S. sclerotiorum* relative to control plants not transformed with the G28 transcription factor transgene (SEQ ID NO:17), and all but one of the lines tested were more tolerant to *B. cinerea* than controls.

11. The Examiner has asserted that Duggleby and Quattrocchio teach that the art of producing a desired phenotype by expression of a nucleic acid sequence encoding a heterologous transcription factor is unpredictable (Examiner's Office action, Paper No. 19, page 9).

It is my considered belief that one of ordinary skill in the art would consider that the teachings of Duggleby and Quattrocchio support the art of expressing a nucleic acid sequence in a transgenic plant to produce a desired phenotype is, in fact, predictable.

Duttleby teaches that one cannot predict the function of proteins encoded by DNAs sequences solely based on homology with another sequence, and that experiments are required in order to evaluate that function. However, Duttleby does not cite any relevant published work to substantiate his statement, and may have based his comment on his experience of enzymes, especially acetolactate synthases (ALS), not transcription factors, the matter of the instant invention claimed by Applicants.

The objective of the studies by Duttleby was to determine whether eukaryotic ALSs contain both small and large subunits, as earlier demonstrated in prokaryotic ALSs, and not only large subunits, as had been earlier suggested by protein purification studies of eukaryotic ALSs. The approach taken by Duttleby was to perform homology searches in GenBank to identify DNA sequences encoding eukaryotic versions of the small subunits. Duttleby teaches the identification of such sequences (Duttleby, Figure 2, page 247). Since experimental evidence of function was not presented in the paper, Duttleby prudently stated that the possibility existed that the algal and yeast sequences identified in GenBank may not encode functional ALS subunits. Duttleby also teaches that the studies so presented "may have significant practical implications" (Duttleby, page 248, column one, fourth paragraph, lines

7-8.)

The major assumption of the study, and the reason it was published in the first place, was that the eukaryotic (algal and yeast) sequences identified based on sequence homology were indeed, more likely than not, to encode small subunits of ALSs, a finding that had not been known earlier. This conclusion was confirmed by Duggleby in a later publication (Pang and Duggleby (1999) Biochemistry 38:5222-5231), which teaches that the yeast sequence described in the 1997 study is indeed the regulatory small subunit of acetolactate synthase.

To further support that the function of sequences identified by homology searches is predictable, Duggleby teaches that homology searches led to identification of some prokaryotic ALS small-subunits in earlier studies. (See Duggleby, page 245, introduction, paragraph bridging column one and two.) It is therefore my considered opinion that one of skill in the art would reasonably believe that the teachings of Duggleby do not present experimental evidence that weakens Applicants' claim that polynucleotides which encode polypeptide conserved domains with a high level of homology to Arabidopsis transcription factor conserved domains are likely be transcription factors of similar function. In fact, Duggleby actually appears to rely on such an assumption in order to identify eukaryotic equivalents of prokaryotic enzymes (see Duggleby, page 248, section 3, note added in proof).

The Examiner has asserted that the teachings of Quattrocchio et al. (1998) demonstrate that one cannot extrapolate the effect of overexpressing a transcription factor from one plant species to another. It is my considered opinion that one of ordinary skill in the art would not interpret the teachings of Quattrocchio thus. Quattrocchio et al. teach that overexpression of specific petunia MYB and HLH genes induce anthocyanin production both in petunia and in corn. Reciprocally, the corn orthologues of the petunia genes produce the same effects in both species (see Quattrocchio, page 481, Figures 6j and 6k; and discussion on page 482, column one, third paragraph). Based on complementation analysis, Quattrocchio teaches that the transcription factors are interchangeable, in terms of the effect they have on anthocyanin accumulation. At the level of gene expression, Quattrocchio teaches that the maize and petunia transcription factors appear to have different effects on the very early genes in the pathway. However, Quattrocchio teaches that it is clearly demonstrable that the effect on the anthocyanin trait in maize of the petunia genes was predictable from overexpression data in petunia. Quattrocchio teaches that this is also true for the maize transcription factor.

Based on the teachings of Quattrocchio and others that describe the effect of Arabidopsis transcription factors in other species (as disclosed below in section 6), it is my considered opinion that one of skill in the art would reasonably believe that modulating expression of transcription factor genes is likely to affect the same trait in Arabidopsis as in other, even distantly related, plant species. It is therefore my considered opinion that one of skill in the art would reasonably believe that the data presented in the teachings of Duggleby and Quattrocchio are not inconsistent with Applicants' claims.

For example, Applicants did not rely exclusively on the annotation of the known database polynucleotide sequence hit; Applicants considered whether the claimed polynucleotides comprised conserved domains known in transcription factors; Applicants found that over-expression of the claimed

polynucleotides in a plant resulted in a modified trait, a characteristic of transcription factors well-known in the art.

It is my considered opinion that one of ordinary skill in the art would have a reasonable expectation that the analyses performed by Applicants and the disclosure by Applicants how to practice the invention is more reliable and more useful in describing how to use the invention than the teachings of Duggleby and Quattroccchio and that the teachings of Duggleby and Quattroccchio are not pertinent to refuting the instant invention.

12. I hereby declare that all statements made herein are true and that they are based on my own knowledge, information and belief. These statements are made with the knowledge that willful false statements are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent issued from it.

Date: 10/18/02

Jacqueline E. Heard

Jacqueline E. Heard, Ph.D.

EXHIBIT A

EID	COMMENT	(0.962)CY3CY5	(0.962)CY3METACOL ROW
E2228	3413711 (AC004747) putative antifungal protein [Arabid... +3 285 17456.72	1280.88	13.629 3 3
E48	2642446 (AC002391) similar to auxin-responsive GH3 pro...+2 39 8425.151	998.9	8.434 2 2
E840	4454029 (AL035394) tyrosine transaminase like protein ...+3 396 2983.997	436.94	6.829 2 4
E132		1501.844	226.31 1 1
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara...+2 33 22878.68	3563.68	6.42 4 4
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSO	26362.1	4325.66 2 3
E5728	2281111 (AC002333) endochitinase isolog [Arabidopsis t...+2 990 3014.765	511.69	5.892 2 2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...+2 564 6490.879	1134.63	5.721 4 3
E2202		6659.916	1285.26 1 3
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin...+1 4 7804.428	1520.45	5.133 2 2
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA...+2 4 15130.91	3007.93	5.03 3 3
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3 396 6170.176	1277.74 4.829 3 3
E4332	G582		420.475 87.24 4.82 1 1
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-...+1 5 4159.393	874.19	4.758 1 2
E3005	3548819 (AC005313) putative heterogeneous nuclear ribo...+1 18 1562.678	336	4.651 1 2
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidops...+3 7 9131.384	2000.7	4.564 4 3
E1220	2894563 (AL021890) putative protein [Arabidopsis thali...+1 293 5989.85	1318.85	4.542 1 3
E4349	G921		788.268 174.04 4.529 1 1
E5432	3193290 (AF069298) contains similarity to a protein ki...+1 415 7 3363.522	760.18	4.425 1 1
E799	1703220 ALG2 PROTEIN >gi 1127806 (U40857) ALG2 [Arabid...+1 9643.615	2197.57	4.388 2 2
E2339		835.638	192.31 4.345 1 2
E6736	3851530 (AF065435) nodulin [Glycine max]	+2 408 2.6 5522.092	1284.91 4.298 4 3
E489		884.1.825	2072.92 4.265 1 1
E4131	A.thaliana cyclophilin	7934.189	1884.34 4.211 4 3
E2684		5655.337	1363.04 4.149 1 2
E3456	1755152 (U75187) germin-like protein [Arabidopsis thal...+3 617 3673.234	888.09	4.136 4 3
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (N	6396.602	1556.82 4.109 2 3
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ...+1 561 1456.033	354.44	4.108 2 1
E772	2460188 (AF020785) polygalacturonase inhibiting protei...+3 316 16190.16	4151.55	3.9 4 3
E618	1946365 (U93215) glutaredoxin isolog [Arabidopsis thal...+2 504 5374.556	1413.26	3.803 3 2
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat...+2 413 15182.26	4017.26	3.779 4 4
E4218		3133.17	830.03 3.775 3 2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...+2 564 6652.197	1766.4	3.766 2 2
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana]	+2 3 2110.749	563.22 3.748 3 4

20	1	3	3	3.707
E4357	G921	31222858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PREC	941.849	254.08
E2367	E2832641 (AL021710) glycolate oxidase - like protein [A... +3	240	6289.9	1721.08
E6149	510876 (X80051) NADP dependent malic enzyme [Phaseoliu...	+1	1566.672	3.655
E2503	E5968 flavonol 4'-sulfotransferase - Flaveria chlora...	+2	6325.547	1
E5968	285286	218	3.4	1
E6710	G1535	2765.031	1745.39	7
E4590	G1006	1372.362	3.604	3
E4844	G8	1372.362	3.599	3
E6757	31222858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PREC	820.278	237.88	5
E4463	E3168	4468044 (X73587) catechol O-methyltransferase [Vanilla...	+1	3.448
E540	E3011	304	1776.11	1
E3857	E540	4587542 (AC006577) Belongs to the PF[00657 Lipase/Acy]...	+3	2
E2546	E3313	3	5167.35	2
E3857	E1758	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f...	+2	2
E2546	E2542	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3	6	17691.61
E3313	E4741	6 17691.61	428.89	5566.58
E1758	E4741	464367 POLYGALACTURONASE INHIBITOR PRECURSOR (PO	2137.109	3.178
E2129600	E5608	2129600 glutathione synthase (EC 6.3.2.3) 2 - Arabidop...	+2	420.648
E3434969	E4461	441	2521.407	676.39
(AB008104)	G10	479.884	146.78	3.16
E1759	E6869	ethylene responsive element binding ... +2	4	394.52
E5608	E5076	4	1282.04	3.25
4581500 (AL034352) putative oxalyl-CoA decarboxylase [...	G28	1	394.52	5566.58
E4461	E822	+1	1282.04	3.25
G10	E28	93	1778.312	3.178
E6869	E5076	1903.34	11704.1	676.39
E5076	E822	1015.848	3706.42	3.16
G28	E822	2025.758	375.74	1
E822	E28	2253.271	3.136	4
E28	E5067	731.81	3.118	4
E5067	E2042	18700.53	3.118	2
E2042	E4275	16453.76	3.087	2
E4275	E1312	1794.897	329.02	6
E1312	E4274	1794.897	329.02	3
E4274	E2049	1798.643	3.079	21
E2049	E6247	1071.72	3.032	17
E6247		1701.813	269.07	22
		579.35	2.968	11
			2.937	4

E2305	12		2	2	1	1	2.915
E4493	G626		199.73	2.913	2.913	2	2.915
E4819	G865		581.822	2.888	2.888	2	2.888
E1564	3434967 (AB008103) ethylene responsive element binding... +1	2	1305.494	452.75	2.883	3	2
E784	3420008 (AF000307) steroid sulfotransferase 3 [Brassic... +1	211	7155.314	2489.64	2.874	4	4
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3	185	2068.364	742.82	2.784	1	1
E6744			2342.621	841.6	2.784	2	2
E2632			9663.652	3506.4	2.756	1	2
E5159			1636.985	600.9	2.724	3	1
E6889	4538929 (AL049483) putative nucleic acid binding prote... +1	132	744.238	273.57	2.72	1	6
E1818	2129733 serine O-acetyltransferase (EC 2.3.1.30) SAT1 ... +1	657	1431.559	530.08	2.701	2	3
E5365			8154.09	3022.76	2.698	3	3
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR		1317.245	494.4	2.664	2	1
E4214	G13		427.356	160.49	2.663	1	2
E2436	2578442 (X67426) pectinesterase [Pisum sativum]	+2	117	4414.864	1667.26	2.648	2
E2444	2578440 (X67425) pectinesterase [Pisum sativum]	+1	147	4195.916	1587.28	2.643	4
E4143	A.thaliana beta tubulin 1		2131.787	809.85	2.632	2	3
E1467	1465368 (X99548) bHLH protein [Arabidopsis thaliana]	+2	223	3113.248	1191.6	2.613	1
E5570	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	212.1	1262.83	484.49	2.607	2
E618	1946365 (U93215) glutaredoxin isolog [Arabidopsis thal... +2	504	6914.53	2658.04	2.601	4	1
E7022			1592.849	614.2	2.593	3	2
E1909			2306.059	889.57	2.592	1	2
E1454	3688186 (AL031804) putative protein [Arabidopsis thali... +3	676	4916.999	1901.77	2.585	2	3
E6521	G7		787.344	304.73	2.584	3	1
E5782	3201612 (AC004669) putative 2A6 protein [Arabidopsis t... +1	316	3381.548	1315.68	2.57	3	3
E4145	A.thaliana beta tubulin 1		1248.009	489.13	2.551	2	2
E1739	1817544 (D83025) proline oxidase precursor [Arabidopsis th... +3	493	1869.656	733.83	2.548	3	2
E4572	G1074		539.217	213.37	2.527	2	3
E1056	4559358 (AC006585) putative steroid binding protein [A... +3	203	2059.212	818.75	2.515	3	4
E1962			1457.15	581.47	2.506	1	4
E2111	2739381 (AC002505) putative patatin [Arabidopsis thali... +2	353	1557.086	624.49	2.493	4	2
E483	2739389 (AC002505) Cf-2.2 like protein [Arabidopsis th... +2	191	17010.14	6825.87	2.492	4	2
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana]	+2	727	3156.499	1269.35	2.487	3
E4591	G263		1919.008	772.91	2.483	4	1
E6748	3540182 (AC004122) Unknown protein [Arabidopsis thaliana] +1	4	931.06	375.07	2.482	2	2

E923	2801536 (AF039531) lysophospholipase homolog [Oryza sativa... +3	1163.116	469.13	2.479	11
E2578	4455220 (AL035440) putative aconitase [Arabidopsis thaliana] +3	194	14524.35	5860.03	2
E2989	2371.224	960.68	2.468	1	2
E2449	3152575 (AC002986) Similar to cytochrome P450tyr gbl U3... +2	1	472.426	191.95	7
E4638	G233	576.443	235.64	2.446	2
E4790	G881	611.782	251.02	2.437	1
E1613	4204303 (AC003027) lcl prt_seq No definition line found... +1	576	5	599.492	4
E4540	G1356	492.492	203.27	2.423	2
E3325	G350	2639.764	1090.71	2.42	1
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida] +2	384	4970.769	2063.86	4
E347	2244949 (Z97339) similarity to ORF - <i>Lilium longiflorum</i> +2	659	1	499.864	16
E4206	G146	432.909	180.44	2.407	2
E5592		4330.778	1812.9	2.399	1
E6897		3872.076	1625.56	2.389	2
E4736	G839	1785.426	751.28	2.377	1
E2982	2584721 (Y10157) sulfite reductase [Arabidopsis thaliana] +1	497	1814.828	763.38	2.377
E5410	4220533 (AL035356) putative mitochondrial uncoupling protein +1	938	445.18	187.63	1
E5814	2342686 (AC000106) Similar to <i>Saccharomyces</i> hypothetical... +3	7	1499.467	634.29	3
E1657	4469019 (AL035602) putative protein [Arabidopsis thaliana] +2	561	1473.559	625.79	18
E6898	4468805 (AL035601) auxin-responsive GH3-like protein [...+1	693	2052.581	873.24	1
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana] +2	2	663.588	284.16	6
E317		856.628	367.33	2.335	1
E5399	2344900 (AC002388) EREBP isolog [Arabidopsis thaliana] +3	5	7468.693	3214.26	4
E3204	3763924 (AC004450) putative extensin [Arabidopsis thaliana] +3	270	2947.782	1271	3
E1756	2344900 (AC002388) EREBP isolog [Arabidopsis thaliana] +1	8	865.376	373.32	14
E884		4327.564	1873.6	2.318	4
E5373	1169544 ERD1 PROTEIN PRECURSOR >pir JN0901 ERD1 prote	9301.787	4030.96	2.308	18
E4050	pathogen-inducible protein CXc750	2339.339	1016.03	2.302	1
E2733		1195.655	521.19	2.294	2
E1265	1703220 AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabidopsis thaliana] +2	1503.076	655.28	2.294	3
E6567		418.387	182.93	2.287	1
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ 3563.077	1059.243	463.67	2.284	1
E4669	G564	1557.64	2.287	4	5
E3003	2642157 (AC003000) ankyrin-like protein [Arabidopsis thaliana] +3	125	909.772	399.63	2.277
E5248	2832641 (AL021710) glycolate oxidase - like protein [Arabidopsis thaliana] +3	288	2287.235	1005.32	2.275

E4005	3' flavonoid O-methyltransferase		2189.117	2.163	2	3	3	18
E1612	1709498 OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pirl S	715.472	333.18	2.147	1	3	3	5
E6792	629602 probable imbibition protein - wild cabbage >em... +3	202	3928.242	1829.23	2.147	2	4	5
G186				412.81	2.143	1	2	21
E4827	2062164 (AC001645) jasmonate inducible protein isolog ... +1	555	8668.39	4044.58	2.143	2	1	18
E1493	3790567 (AF078821) RING-H2 finger protein RHA1b [Arabi... +2	6	1306.014	610.04	2.141	1	4	15
E3396				844.14	2.14	2	1	11
E2019	G351			233.21	2.139	1	1	6
E6890				468.807	219.64	2.134	4	1
E4899				2605.29	1221.45	2.133	2	10
E694				1529.552	717.99	2.131	1	12
E2183	2493391 PROBABLE STERIGMATOCYSTIN BIOSYNTHESIS P45	750.474	352.13	2.131	3	1	1	12
E5069	G189			2848.664	1337.67	2.13	4	5
E6340				5407.104	2539.95	2.129	4	3
E6768	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +2	6	1544.392	726.33	2.126	3	1	18
E1607	4337192 (AC006403) hypothetical protein [Arabidopsis t... +1	279	956.42	451.09	2.12	2	1	4
E6325	3549626 (AJ009696) wall-associated kinase 1 [Arabidops... +3	56	21140.26	10013.22	2.111	4	4	11
E2108				1091.08	518.8	2.103	1	7
E2497	3335363 (AC003028) hypothetical protein [Arabidopsis t... +1	414	3360.856	1601.09	2.099	3	2	7
E2690				558.282	266.08	2.098	1	3
E5742				769.299	366.85	2.097	3	21
E4745	G771			1554.4	2.096	2	1	13
E3087	4263715 (AC006223) putative alanine acetyl transferase... +3	616	3258.543	7230.46	2.093	4	1	14
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Ara... +2	630	5	15133.8	895.61	2.091	2	3
E5942	3044214 (AF057044) acyl-CoA oxidase [Arabidopsis thali... +1	46	1872.495	1488.332	712.87	2.088	1	4
E6199				502.058	240.53	2.087	2	4
E6013				853.308	408.85	2.087	3	6
E6595	3399769 (U76299) uclacyanin II [Arabidopsis thaliana]	+3	645	2611.25	2.086	2	1	18
E3253	2252844 (AF013293) belongs to the cytochrome p450 fami... +3	5	5446.938	1570.31	755.61	2.078	1	21
E5132				2825.989	1360.72	2.077	1	3
E932	G179			663.771	319.8	2.076	2	7
E2692	3115108 (AJ223983) plant uncoupling mitochondrial prot... +3	325	7786.864	3747.23	2.078	1	3	11
E5560	1708463 IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) I...			917.47	2.072	1	2	2
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3	462	5346.983	2578.95	2.073	3	3	16
E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabid... +2			901.098	1279.557	2.055	2	2
E4604	G452			622.68				

E2809	3668086 (AC004667) unknown protein [Arabidopsis thaliana] +2 1	7060.96	3450.37	2.046
E2768	4522009 (AC007069) unknown protein [Arabidopsis thaliana] +3 6	5992.959	2939.04	2.039
E4279		495.755	243.25	2.038
E1229		504.965	248.23	2.034
E1465		1214.883	597.15	2.034
E2141	2160189 (AC000132) Similar to A. thaliana receptor-li... +2	130 2 1576.998	1658.36	2.034
E3077		609.01	778.16	2.027
E2755		301.59	2019	1
E6408	4587526 (AC007060) Strong similarity to F1913.2.gi 303... +1	255	6484.825	3211.54
E5534	3702317 (AC005397) unknown protein [Arabidopsis thalia... +3	35	2098.738	1040.11
E3736	1695719 (D89342) luminal binding protein [Arabidopsis ... +1	773	17274.69	8566.57
E709		5121.048	2541.92	2.017
E1280	1171866 NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUN 2403.628		1194.5	2.012
E6319	1708971 (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSO		224.33	2.009
E2340	4249390 (AC005966) Similar to gbj AF039182 probable aid... +1	1	1664.837	830.73
E5824	1617274 (Z72152) AMP-binding protein [Brassica napus] +3	48	482.801	241.01
E1278		4257.732	2129.21	2
E5354	3935145 (AC005106) T25N20.9 [Arabidopsis thaliana] +1	277	629.048	314.8
E5789	4585983 (AC005287) Unknown protein [Arabidopsis thaliana] +3	3	1008.476	504.9
E4324	G501		1115.573	558.87
E1491	3193289 (AF069298) similar to several small proteins (... +1	415	1432.82	718.43
E4460	G4		732.882	368
E1742	3080447 (AL022605) putative protein [Arabidopsis thali... +1	250	419.955	211.04
E6291		878.455	441.74	1.99
E808	2832649 (AL021710) adenylosuccinate lyase - like prote... +2	250	17468.7	8782.61
E5681	2281111 (AC002333) endochitinase isolog [Arabidopsis t... +2	775	1831.92	921.58
E2627		8133.542	4097.73	1.985
E614		9547.846	4810.06	1.985
E6415	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ 5706.557		2880.97	1.981
E1166	1353163 HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHRO		661.779	334.28
E6153	3892722 (AL033545) putative protein [Arabidopsis thali... +1	262	581.88	294
E2154	3913518 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-... +3		1123.407	568.98
E3393	2653885 (AF027408) phospholipase D-gamma; PLD-gamma [A... +		792.705	402.66
E968	585960 PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUN		1027.503	521.86
E2706		14849.41	7554.28	1.966

EXHIBIT B

EID	COMMENT	(0.845)CY5	(0.845)CY3: METAROY	METACOL ROW
E2228	3413711 (AC004747) putative antifungal protein [Arabid... +3 285 2.8 26241.51	934.58	28.078	3
E48	2642446 (AC002391) similar to auxin-responsive GH3 pro... +2 390 4 22679.91	1008.78	22.483	2
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR- 5345.965	245.81	21.748	2
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana] +3 330 1.2 20977.1	1046.73	20.041	3
E2692	1708463 IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) 1...+1 8625.171	548.85	15.715	1
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3 396 4.€ 5600.37	3622.92	15.431	2
E3855	4099847 (U90523) saccharopine dehydrogenase [Arabidops... +3 65€ 4998.476	348.2	14.355	1
E5728	2281111 (AC002333) endochitinase isolog [Arabidopsis t... +2 990 5. 3633.133	264.47	13.737	2
E2632		13960.51	1089.66	12.812
E2339			1089.66	12.812
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Ara... +2 630 5.2e- 27910.36	155.97	12.017	1
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	2555.41	10.922	4
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thalian... +3 493 2.6€ 4940.54	3636.445	345.23	10.533
E4579	G1329	565.646	60.68	9.322
E6646	3164144 (D78607) cytochrome P450 monooxygenase [Arabid... +1 3(1978.575	227.02	8.715	1
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	1832.329	213.28	8.591
E6757	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURS	6416.669	753.41	8.517
E2202	1064887 (X92955) pollen coat protein [Brassica oleracea] +3 287 1.; 2070.147	6417.184	761.45	8.428
E337	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2 428 29303.86	253.51	8.166	2
E2230		3656.44	8.014	3
E6710		1625.231	202.96	8.008
E4741	G759	1367.624	182.43	7.997
E4540	G1356	997.889	140.27	7.114
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1 561 8.€ 1437.026	209.08	6.873	2
E2493		5311.873	779.18	6.817
E132		2126.005	326.34	6.515
E1909		4038.617	634.67	6.363
E2367	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURS	6550.174	1040.77	6.294
E5432	3193290 (AF069298) contains similarity to a protein ki... +1 415 7.0e- 2909.183	464.07	6.269	1
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	1357.147	220.68	6.15
E508		10058.84	1642.78	6.123
E822		6187.663	1024.78	6.038
E6869	2281113 (AC002333) endochitinase isolog [Arabidopsis t... +1 581 2. 2052.945	2052.945	350.49	5.857
E5145				185.61
E4522				1076.213
E4064	cinnamyl alcohol dehydrogenase			1160.848
				201.3
				5.767
				4.10
				2.2
				1.1
				0.6
				22
				1
				3
				20

E2044	G413	cinnamyl alcohol dehydrogenase	9413.741	1439.94	5.705	11	1	2	2	4	5.603	9
E4064			12511.85	2240.82	5.584	1	1	1	1	2	5.579	1
E489			5214.361	934.57	5.579	1	2	1	1	2	5.526	2
E4056		PUTATIVE TRYPsin INHIBITOR T01O24.25 PRECURSOR	10606.56	1919.37	5.526	10	2	2	2	2	5.473	1
E799		1703220 AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabid... +1 1	5381.908	983.37	5.473	9	1	1	1	1	5.36	1
E540		4587542 (AC006577) Belongs to the PF 00657 Lipase/Acyl... +3 372	4492.811	838.27	5.36	18	2	2	2	2	5.298	1
E1753		4388726 (AC006413) putative 12-oxophytodienoate-10,11... +1 528	781.235	147.46	5.298	19	2	2	2	2	5.16	2
E4443	G413	2347199 (AC002338) protein kinase isolog [Arabidopsis ... +3 464 3	1605.578	311.18	5.16	16	2	2	2	2	5.153	2
E1025		3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (I	27153.38	5269.4	5.067	12	2	3	3	3	5.067	1
E741		2708482 (U79556) IAA25 [Arabidopsis thaliana]	+3 524 1.3e-	2395.347	472.78	12	2	2	2	2	4.975	2
E2353		2829900 (AC002311) similar to ripening-induced protein... +3 610 1.7	1591.958	319.97	4.959	2	2	2	2	2	4.959	1
E5688		10905.2	2199.04	4.959	4	16	1	1	1	1	4.842	2
E1107		4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1 438	8106.207	1674.02	4.842	10	2	2	2	2	4.763	3
E861		cinnamyl alcohol dehydrogenase	3202.048	672.23	4.763	10	2	2	2	2	4.724	3
E4064		3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2 380	3115.934	659.56	4.724	18	2	2	2	2	4.708	3
E1704		4589123 (AF126374) At14a protein [Arabidopsis thaliana]	+1 566 4.	5073.818	1077.72	19	2	2	2	2	4.691	4
E1783		2460188 (AF020785) polygalacturonase inhibiting protei... +3 316 7.7	9696.348	2067.18	4.691	10	3	3	3	3	4.683	1
E772		4939.265	1054.72	4.683	1	12	2	2	2	2	4.623	2
E2305		11382.47	2462.16	4.623	1	16	2	2	2	2	4.614	1
E1114	G1745	1709498 OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pir S57...	922.894	200.04	4.614	18	3	3	3	3	4.611	2
E1612		A.thaliana beta tubulin 1	1241.157	269.19	4.611	22	3	3	3	3	4.558	1
E4143		3738340 (AC005170) GMP synthase-like protein [Arabidop... +2 472	2114.581	463.92	4.558	17	2	2	2	2	4.539	4
E1312		G242	8600.677	1894.92	4.539	10	3	3	3	3	4.5	1
E725		4117381 NITRILASE 1 >pir S22398 nitrilase (EC 3.5.5.1... +2 530 3.1	4137.396	919.32	4.5	15	1	1	1	1	4.458	3
E3566		629602 probable imbibition protein - wild cabbage >em... +1 256 4.2	24401.53	5473.63	4.458	7	2	2	2	2	4.409	3
E2698		584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +3 698 9	7016.585	1591.59	4.409	5	2	2	2	2	4.405	4
E6637		6661.746	1512.23	4.405	1	1	1	1	1	1	4.393	3
E4064		2493391 PROBABLE STERIGMATEOCYSTIN BIOSYNTHESIS P450 N	2111.033	480.57	4.393	12	1	1	1	1	4.383	4
E2183		E610	3202.226	730.62	4.383	20	2	2	2	2	4.344	1
E4617		2674.668	615.73	4.344	11	4	4	4	4	4	4.33	3
E1962		811.272	187.36	4.33	21	3	3	3	3	3	4.329	1
E4745	G771	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f... +2 1:	1101.239	254.36	4.329	16	3	3	3	3	4.308	1
E3857		E2684	4195.941	974.06	4.308	7	2	2	2	2	4.276	4
E3703		2880054 (AC002340) putative cytochrome P450 [Arabidops... +3 745 11312.49	2645.42	4.261	4.248	15	3	3	3	3	4.248	2
E3168		E1465	3545.727	834.59	4.248	17	1	1	1	1	4.248	1

17	E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana]	+3	491	4.2.	8204.91	1935.13
4	E6149	2832641 (AL021710) glycolate oxidase - like protein [A...+3	240	2.1e	1413.546	334.64	4.24
1	E2065	3810848 (AL032684) putative autophagy protein [Schizosaccharomyces pombe]	+1	214	9	2975.391	4.224
1	E775	4432837 (AC006283) hypothetical protein [Arabidopsis thaliana]	+3	314	2.4	12648.89	2
2	E329	4262182 (AC005508) 44123 [Arabidopsis thaliana]	+1	426	6.6e	10566.64	4.223
9	E2291	4432835 (AC006283) unknown protein [Arabidopsis thaliana]	+1	155		3683.769	2
1	E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabidopsis thaliana]	+2	7f		2166.02	12
2	E1654	1762933 (U66263) tumor-related protein [Nicotiana tabacum]	+3	178	1.5	5462.564	2
3	E2740					1313.58	2
3	E6138					4.159	18
1	E1431					3	18
1	E5447	2342687 (AC000106) Similar to Beta integral membrane protein [Arabidopsis thaliana]	+3	510		837.904	13
1	E4827	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3	396	2.4	202.35	13
3	G186					4.141	4
3	E6759	2827709 (AL021684) predicted protein [Arabidopsis thaliana]	+1	272	2.1	1520.96	17
1	E1594	4559366 (AC006585) putative tyrosine transaminase [Arabidopsis thaliana]	+2	335	2	7026.91	3
2	E4337					1745.58	3
2	E2084	4587610 (AC006951) putative indole-3-glycerol phosphatase [Arabidopsis thaliana]	+2	413	5.	406.037	21
4	E2628	1946364 (U93215) lipase isolog [Arabidopsis thaliana]	+2	391	6.0e	3186.037	21
4	E6708					806.14	21
4	E5229	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	182	2.0e-	12648.747	21
2	E2678	1181531 (L41244) thionin [Arabidopsis thaliana] >pf1 ...+2	430	7.9e-	12602.09	321.09	21
3	E2153					328.368	21
2	E1093	2194118 (AC002062) F20P5.4 gene product [Arabidopsis thaliana]	+1	326		85.04	20
2	E6975	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+2	694	2.4e	322.3	20
1	E4145	A.thaliana beta tubulin 1				940.646	18
1	E6898	4468805 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]	+1	693	1.	841.419	18
1	E4505					2677.938	18
6	E4265	G773				710.051	18
2	E5529	G255				188.39	18
2	E5592	2583108 (AC002387) putative surface protein [Arachis hypogaea]	+2	403	:	2151.454	18
2	E1950	1491776 (M37636) cationic peroxidase [Arachis hypogaea]	+2	602	1.	572.93	18
1	E4026					4747.747	18
1	E4687					1268.47	18
1	E4131	G663				3942.821	18
1	E6340	A.thaliana cyclophilin				526.113	18
1	E5681	2281111 (AC002333) endochitinase isolog [Arabidopsis thaliana]	+2	775	3.	621.816	18
5	E5544	2190555 (AC001229) No definition line found [Arabidopsis thaliana]	+2	252	1:	2720.868	18
2						4114.71	18

E6581	4337027 (AF123254) MFP2 [Arabidopsis thaliana]	+1	207	6.9e	1511.767	411.75	6	1	1	18
E1451	2911039 (AL021961) cinnamyl alcohol dehydrogenase - li...	+3	513	6	9788.639	2674.95	3.659	4	1	1
E5493	2065013 (Y11650) cyclic phosphodiesterase [Arabidopsis...]	+2	796	4	4214.216	1156.65	3.643	3	2	2
E1056	4559358 (AC006585) putative steroid binding protein [A...	+3	203	1.4	2258.124	624.94	3.613	3	4	17
E5365	1009712 (U27698) calreticulin [Arabidopsis thaliana]	+2	611	8.0e-	10975.95	3048.66	3.6	3	3	2
E6471	1009712 (U27698) calreticulin [Arabidopsis thaliana]	+2	611	8.0e-	5768.686	1606.91	3.59	2	2	4
E884	G681				6483.037	1807.27	3.587	1	3	11
E4728	E3308	849074 (D50737) B-type cyclin [Nicotiana tabacum]	+1	126	9.2e	728.766	204.38	3.566	1	2
E3736	E3308	1695719 (D89342) luminal binding protein [Arabidopsis ...]	+1	773	5.4	15678.82	4406.35	3.558	4	3
E4432	E562	E5593	4309731 (AC006439) hypothetical protein [Arabidopsis t...	+2	216	6.C	1237.659	349.21	3.554	1
E5623	E6768	E3069	3367517 (AC004392) Similar to F411.26 putative beta-gl...	+2	697	6.1	8544.482	2440.28	3.501	2
E1865	E6635	E2500	2829898 (AC002311) Hypothetical protein [Arabidopsis t...	+2	594	5.	1129.679	327.36	3.451	1
E1362106	E586	E6342	1362106 GUT 7-2a protein - common tobacco (fragment)	+3	283	14067.35	4090.82	3.439	3	7
E2598597	E1657	E4242	2598597 (Y15371) MTN5 [Medicago truncatula]	+2	181	3.0e-	2695.157	785.17	3.433	1
E3319340	E179	E4591	3319340 (AF077407) contains similarity to E. coli cati...	+1	187	5.9e-	6024.019	1767.63	3.408	2
E4469019	E263	E4270	4469019 (AL035602) putative protein [Arabidopsis thali...	+2	561	1.6e	2096.433	616.22	3.402	1
G358	E5248	E3859	G358	E5248	E5248	E5248	E5248	E5248	E5248	E5248
E4662633	E1374	E932	4662633 (AC007267) hypothetical protein [Arabidopsis t...	+3	263	6.C	2088.702	615.2	3.395	1
G263	E1374	E932	G263	E1374	E932	E2323	E5640	E280	E5640	E280
E4591	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
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G39	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
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E5468	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
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E4945	E1374	E932	E4270	E1374	E932	E2323	E5640	E280	E5640	E280
E2880	E1374	E932	E4270	E1374	E932	E2323</td				

E1525	2160152 (AC000375) ESTs gblU75592.gb T13956,gb T43869 ... +2 4	1193.952	372.08	17	16
E986	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23.	1642.873	514.32	2	2
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S66354 ... +	9025.839	2829.33	3	1
E6297	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e...	+2 240 1	10103.31	3167.04	8
E2340	4249390 (AC005966) Similar to gb AF039182 probable aid... +1	178	2099.542	659.45	5
E2733		1145.47	359.92	3.194	12
E417	4406765 (AC006836) putative cold-regulated protein cor... +3	458 1.	569.71	179.07	13
E1935	4210330 (AJ223802) 2-oxoglutarate dehydrogenase, E1 su... +2	408	3925.086	1233.81	9
E1554	1170247 HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U018... .	2130.305	670.85	3.176	11
E6133		1012.557	320.47	3.16	4
E3834	729470 MITOCHONDRIAL FORMATE DEHYDROGENASE PRECUR	7973.141	2527.07	3.155	17
E5223	1403134 (X98453) peroxidase [Arabidopsis thaliana]	+3 485 1.8e	2195.854	697.49	16
E657	629670 hypothetical protein - tomato	+2 422 8.5e-39	1	2718.638	4
E4431	G515		881.493	863.72	10
E2137	3164222 (AB008518) RMA1 [Arabidopsis thaliana] >gi 420...	+1 413	5228.243	280.69	19
E971		3192.568	1669.59	3.14	12
E6211	G242	1413.013	1669.59	3.131	11
E5773	3894194 (AC005662) putative strictosidine synthase [Ar...	+2 742 1.1	934.706	2.2	16
E242	4454461 (AC006234) putative cell wall protein precursor... +2	593 6.5	629.074	3.106	5
E516	2281627 (AF003094) AP2 domain containing protein RAP2... +2	764	7886.444	404.02	3
E5325	3859607 (AF104919) contains similarity to cysteine pro... +3	329 6.3e	1888.651	2561.22	9
E3553	4544458 (AC006592) unknown protein [Arabidopsis thaliana]-1	593	614.07	3.079	10
E6743	3540182 (AC004122) Unknown protein [Arabidopsis thaliana] +3	823	1296.989	3.076	7
E514	2462824 (AF000657) similar to Jun activation domain bi... +2	740 2.4	1027.638	422.39	15
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23.	3491.441	964.35	336.24	5
E1013		1144.13	964.35	3.056	10
E2578	4455220 (AL035440) putative aconitase [Arabidopsis tha... +3	194 2.	11752.62	1144.13	3
E5434	3334124 ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECU	926.789	1858.2	611.58	4
E6013		632.986	3887.31	3.052	16
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISO2	2558.915	608 1.7	3.038	12
E5984	3236255 (AC004684) hypothetical protein [Arabidopsis t... +2 115 3.e	2894.085	849.02	3.023	2
E1278		4515.97	962.16	3.018	2
E6110	4115383 (AC005967) receptor-like protein kinase [Arabi...	+1 608 1.7	967.72	306.78	1
E6649	544256 ESTERASE FE4 PRECURSOR (CARBOXYLIC-ESTER HYD)	1772.644	934.01	2.992	4
E3753	2062156 (AC001645) jasmonate inducible protein isolog ... +2	580 1.	2890.485	2.989	6
E6409		3534.836	967.72	2.987	15
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3	185 1.2e	1005.594	1186.38	2
			338.26	2.973	4
			2.973	1	12

EXHIBIT C

EID	COMMENT	(1.243)CY3	CY5	CY5/(1.243)CY3 SOURCE
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR OF	827.813	37800.35	45.663 L20P15F02,L35P91G09
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis t... +1 ξ	316.816	10493.82	33.123 L18P29E04,L35P88H06
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida](germinating) I	613.619	15984.65	26.05 L17P17D04,L35P107H01
E2050		1354.82	30604.31	22.589 L20P13A01,L35P91D10
E3171	481821 probable glutathione transferase (EC 2.5.1.18)... +3 - 58	1805.183	32667.3	18.096 L15P4C09,L35P101E03
E5077	G354	260.781	3452.33	13.238 J129B10F1
E1197		409.892	5347.98	13.047 L18P10G01,L35P112F07
E5291		236.307	2837.19	12.006 J56A10F1
E2788	1523796 (X97864) cytochrome P450 [Arabidopsis thaliana] +1	817.956	9539.21	11.662 L23P5G04,L35P97C07
E4570	G1043	688.51	8022.4	11.652 J123D08F1
E1106	2129634 lectin-like protein - Arabidopsis thaliana >em... +1 426	1484.154	14031.72	9.454 L17P3E09,L35P111B08
E4564	G920	554.987	5000.25	9.01 J123C06F1
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat... +2 -	1567.895	14004.82	8.932 L20P17H02,L35P92B02
E501	4115383 (AC005967) receptor-like protein kinase [Arabi... +1 1{	1215.952	10226.37	8.41 L17P32C01,L35P85C01
E2108	3549626 (AJ009696) wall-associated kinase 1 [Arabidops... +3	3415.427	28051.43	8.213 L20P2G11,L35P92F02
E1374	4725948 (AL049730) putative Phospholipase D [Arabidops... +3	211.459	1685.88	7.973 L18P33H09,L35P114C12
E2049	3851530 (AF065435) nodulin [Glycine max]	+3 640 {	1105.126	7.753 L20P12H08,L35P91D09
E1491	3193289 (AF069298) similar to several small proteins (... +1 41:	1014.039	7710.42	7.604 L20P16E07,L35P115G09
E3173	3241945 (AC004625) unknown protein [Arabidopsis thaliana] +2	1080.999	8143.19	7.533 L15P4D01,L35P101E05
E2737	4115914 (AF118222) contains similarity to Iron/Ascorba... (oxidic	1083.299	8023.51	7.407 L23P2E08,L35P97B04
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1 29:	498.182	3485.66	6.997 L18P1D03,L35P113A06
E764	3608142 (AC005314) putative hin1 [Arabidopsis thaliana]	+1 1	1277.244	8309.28
E250	2618727 (U49075) IAA19 [Arabidopsis thaliana]	+2 334	906.955	6.506 L18P15H06,L35P87G08
E4450	G354	141.217	906.06	6.457 L17P17D08,L35P82A07
E1466	3883128 (AF082302) arabinogalactan-protein [Arabidopsi... +2	333.186	2121.66	6.416 J122C12F1
E2109	2052383 (U66345) calreticulin [Arabidopsis thaliana]	+1 477	3952.602	6.368 L20P10A05,L35P115C08
E1080		1031.615	6493.24	6.343 L20P2H03,L35P92F03
E3748	4324714 (AF110771) ammonium transporter [Arabidopsis t... +1	3181.631	19053.99	6.294 L17P41F08,L35P111D04
E4790	G881	299.227	1768.78	5.989 L17P17F09,L35P107H08
E1909		2874.859	17006.95	5.949 J126C04F1
E6546		404.82	2350.01	5.916 L18P5C02,L35P90E01
E4591	G263			5.911 J44B06F1
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3 18:	1047.028	6060.78	5.805 J124B01F1
E2533		301.925	1743.19	5.789 L22P12B01,L35P93G03
E4737	G271	1043.56	6016.65	5.774 L15P7B11,L35P77G11
E1460	3451056 (AL031326) serine/threonine kinase - like prot... +1 19	1022.641	5735.08	5.766 J125G04F1
				5.608 L18P8F11,L35P115B08

E3736	1695719 (D89342) luminal binding protein [Arabidopsis ... +1	77	2829.067	15827.06	5.594 L17P16D02,L35P107D08
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidops... +3		1164.715	6491.31	5.573 L17P16C08,L35P107D06
E1843			841.946	4669.77	5.546 L24P12H04,L35P119B07
E1465			895.519	4883.32	5.453 L20P10A03,L35P115C07
E4418	G1417		105.469	573.32	5.436 J122F04F1
E1807	4741198 (AL049746) putative protein [Arabidopsis thali... +2	46	790.498	4187.03	5.297 L24P5F09,L35P119D01
E2086			2232.315	11762.04	5.269 L20P1A01,L35P92B04
E1867	2435406 (U83490) thaumatin-like protein [Arabidopsis t... +2	57	708.721	3730.18	5.263 L28P1F06,L35P119F07
E2059	2924777 (AC002334) putative receptor protein kinase [A... +2	1	972.287	5061.03	5.205 L20P14E08,L35P91F07
E586	2598597 (Y15371) MtN5 (nodulin) [Medicago truncatula]		1540.599	8007.6	5.198 L17P3F04,L35P86A03
E2968			1552.158	8058.3	5.192 L24P5H11,L35P98A10
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC		1221.11	6300.68	5.16 L20P14B07,L35P91E10
E3226	4262180 (AC005508) 29621 [Arabidopsis thaliana] +2	62	2620.79	13519.8	5.159 L15P4F04,L35P101F10
E3478	322551 nucleoside-diphosphate kinase (EC 2.7.4.6) - A... +1	4:	2990.607	15420.6	5.156 L16P10C07,L35P103E12
E4761	G1048		602.668	3045.46	5.053 J125D07F1
E3848			989.055	4966.92	5.022 L17P21F07,L35P109B01
E1454	3688186 (AL031804) putative protein [Arabidopsis thali... +3	67	1204.616	5951.48	4.941 L18P6F12,L35P115A08
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3	4	717.646	3514.61	4.897 L17P21G01,L35P109B04
E5067			422.868	2066.26	4.886 J129A09F1
E2551			1396.199	6808.46	4.876 L22P8E01,L35P96B05
E4827	G186		167.196	813.94	4.868 J126C05F1
E2724	1174498 SYNAPTOBREVIN-RELATED PROTEIN >gii600710 (N		2295.584	11050.18	4.814 L16P1A07,L35P78H09
E4329	G536		847.49	4048.24	4.777 J121D11F1
E2807			729.902	3457.74	4.737 L24P12H08,L35P97F11
E4356	G993		660.555	3107.25	4.704 J121H01F1
E567			1882.97	8834.27	4.692 L17P37H03,L35P85F08
E2111	2739381 (AC002505) putative patatin (storage protein) [Arabidop		3224.552	15064.2	4.672 L20P2H07,L35P92F05
E1011	4263818 (AC006067) unknown protein [Arabidopsis thaliana] +3		969.254	4524.51	4.668 L17P37F07,L35P110H04
E4918	G348		224.958	1048.51	4.661 J127F10F1
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2		1303.496	6015.49	4.615 L22P7D12,L35P118B06
E4108	GP-39		281.738	1293.53	4.591 O17202,M80927
E2256			1313.117	5988.01	4.56 L22P11F05,L35P93F12
E4324	G501		559.138	2527.11	4.52 J121D01F1
E5069	G189		407.269	1839.87	4.518 J129A10F1
E3683	1170505 EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)>		967.377	4351.28	4.498 L17P13G06,L35P107A02
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thaliana... +3	49:	1570.12	7037.43	4.482 L17P27B07,L35P109H01
E3728	4490728 (AL035709) putative protein [Arabidopsis thali... +1	51:	1568.864	7000.53	4.462 L17P15D09,L35P107B11

E1455	128188 NITRATE REDUCTASE 2 (NR2) >pir RDMUNH nitrate	2636.937	11752.94	4.457 L18P6G08,L35P115A09
E4345	G867	1878.881	8286.92	4.411 J12F11F1
E6768		1191.937	5161.98	4.331 J46F06F1
E4051	NITRATE REDUCTASE 2	1006.867	4332.01	4.302 L18P6G08F1
E3476		846.172	3610.37	4.267 L16P10C02,L35P103E10
E1714	2914705 (AC003974) putative disease resistance protein... +1 ζ	889.689	3792.26	4.262 L22P9A11,L35P118D04
E1450	2914705 (AC003974) putative disease resistance protein... +1 ζ	436.392	1851.87	4.244 L20P17C01,L35P115H04
E3704	625977 (ribosome associated) p40 protein homolog - Arabidof	2388.536	10120.36	4.237 L17P16D11,L35P107E01
E1962		2509.318	10594.89	4.222 L18P5H12,L35P90E12
E4349	G921	644.035	2699.53	4.192 J121G09F1
E4514	G986	121.466	501.9	4.132 J123C12F1
E3578	4406816 (AC006201) 60S ribosomal protein L2 [Arabidops... +1	2857.905	11804.49	4.13 L16P5H09,L35P105G07
E2914		1163.037	4784.6	4.114 L16P5H12,L35P79H10
E4051	NITRATE REDUCTASE 2	1845.842	7556.55	4.094 L18P6G08F1
E3430	3687251 (AC005169) unknown protein [Arabidopsis thaliana] +1	672.811	2726.26	4.052 L16P10A11,L35P103E06
E3698	4582468 (AC007071) putative 40S ribosomal protein; con... +1	1421.308	5750.34	4.046 L17P15G01,L35P107C05
E3711	4506685 ribosomal protein S13 >sp Q02546 RS13 _ HUMAN 40..	1670.517	6739.3	4.034 L17P17B02,L35P107G02
E3727	3036808 (AL022373) DnaJ-like protein [Arabidopsis thal... +2 5	3228.231	12983.32	4.022 L17P15D06,L35P107B10
E3422	1350707 60S RIBOSOMAL PROTEIN L29 >pir JC2012 ribosom	1136.164	4557.43	4.011 L15P9F02,L35P103D04
E5011		214.007	855.56	3.998 J128B05F1
E2382	2213626 (AC00103) F21J9.18 [Arabidopsis thaliana]	+2 4	966.01	3846.92
E2367	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRF		3569.062	14193.76
E2684		1927.656	7643.96	3.977 L22P2A02,L35P95C02
E1287	G742	1943.169	7689.49	3.965 L15P8B11,L35P78A11
E4051	NITRATE REDUCTASE 2	945.587	3738.56	3.957 L18P28C09,L35P113E07
E3225	730526 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOI	2407.752	9514.55	3.954 L18P6G08F1
E2759	G415	489.008	1909.65	3.952 L15P4F03,L35P101F09
E3699	2576363 (U39783) amino acid transport protein [Arabido... +3 5	311.11	1212.88	3.905 L24P10G03,L35P97F02
E3447	3123279 40S RIBOSOMAL PROTEIN S26 >gi 2651298 (AC0022	1007.948	3920.42	3.899 L17P15G07,L35P107C06
E2857	4455210 (AL035440) putative aspartate-tRNA ligase [Ara... +3 ;	1187.052	4605.89	3.88 L16P11D03,L35P103H05
E1525	2160152 (AC00375) ESTs gbl U75592,gbl T13956,gbl T43869 ...	403.154	1561.66	3.874 L20P7B02,L35P116E01
E2771	1703227 ALANINE AMINO TRANSFERASE 2 (GPT) (GLUTAM...	2775.904	10751.83	3.873 L24P2D05,L35P97H02
E4069	caffein o-methyltransferase	472.974	1826.18	3.861 L34P4G06F1
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER	1654.109	6386.55	3.861 L17P17F09F1
E3187	1710780 40S RIBOSOMAL PROTEIN S9 (S7) >emb CAA65433	2046.537	7871.84	3.846 L15P4H08,L35P101H01
E2774	3021269 (AL022347) putative protein [Arabidopsis thali... +1 41:	2969.688	11418.22	3.845 L24P2E06,L35P97H05
E3901	4512675 (AC006931) putative citrate synthase [Arabidop... +2 5	1053.131	4012.78	3.81 L17P22B10,L35P109B12

E4912	G1113	3.802 J127E11F1
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURS	3.786 L17P9G05,L35P87C08
E1652	4206789 (AF112864) syntaxin-related protein At-SYR1 [A... +2]	3.759 L22P13F02,L35P117B08
E5132	G179	3.758 J129A08F1
E3729	3702339 (AC005397) unknown protein [Arabidopsis thaliana] +2	3.739 L17P15E02,L35P107B12
E1688	4490297 (AL035678) putative protein [Arabidopsis thali... +1 27.	3.726 L22P2B03,L35P117H08
E3801	1619300 (X95269) LRR protein [Lycopersicon esculentum] +2	3.713 L17P18C12,L35P108A10
E670	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2	3.706 L17P7B05,L35P86G09
E3247	2369714 (Z97178) elongation factor 2 [Beta vulgaris] +1 491	3.695 L33P7H04,L35P120B01
E2990		3.69 L28P3C02,L35P98E08
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER	3.682 L17P17F09F1
E1456	1172599 PROTEASOME COMPONENT C5 (MULTICATALYTIC	3.644 L18P6H10,L35P115A10
E2556		3.625 L22P8G08,L35P96C04
E4344	G763	3.615 J121F03F1
E1440	4512699 (AC006569) putative NADH-ubiquinone oxidoreducta... +1	3.613 L20P14F06,L35P115F06
E4384	G776	3.609 J121F05F1
E2531	3461828 (AC004138) unknown protein [Arabidopsis thaliana] +1	3.607 L15P7A12,L35P77G09
E4110	GP-39	3.596 O17204,M80927
E3216	4539292 (AL049480) putative ribosomal protein S10 [Ara... +3]	3.566 L15P4C04,L35P101D12
E1223		3.551 L18P20F12,L35P113B03
E4192	A.thaliana transcriptional activator CBF1 mRNA,	3.55 O17292,U77378
E718	2499087 UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANS	3.546 L18P15F01,L35P87G03
E146	G364	3.528 L17P16D07,L35P81G05
E2325	4585972 (AC005287) Putative ATPase [Arabidopsis thaliana] +1	3.524 L22P17B04,L35P94B10
E3554	4185509 (AF102821) actin depolymerizing factor 3 [Arab... +3 6	3.515 L16P5E08,L35P105E05
E2527	464720 40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) .	3.512 L15P6B11,L35P77F11
E646		3.511 L17P41E06,L35P86C09
E4378	G531	3.509 J121D07F1
E2112	G286	3.5 L20P4B03,L35P92F06
E1412		3.483 L18P7D04,L35P115B02
E3685	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi... +3	3.483 L17P14A11,L35P107A04
E3734		3.483 L17P16A04,L35P107C11
E3827	2245110 (Z97343) hypothetical protein [Arabidopsis tha... +2 31	3.483 L17P3D04,L35P108F07
E1066	1922937 (AC000106) Similar to Glycine SRC2 (gb AB00013... +2	3.465 L17P3D04,L35P111B01
E2008	4455800 (Z97343) unnamed protein product [Arabidopsis ... +3	3.462 L20P13E01,L35P91E04
E1414	4263710 (AC006223) (TF not in Tfgene) HOX-like? putative pu	3.452 L18P7G02,L35P115B04
E3856		3.448 L17P22D03,L35P109C03

E1419	2341034 (AC000104) F19P19.13 [Arabidopsis thaliana]	+1	·	4039.798	13926.87		
E3922	1086263 TMV resistance protein N - tobacco (Nicotiana ... +3	2	·	581.425	2002.08	3.447 L18P9E05,L35P115CC03	
E1818	2129733 serine O-acetyltransferase (EC 2.3.1.30) SAT1 ... +1	€	·	3754.306	12918.94	3.443 L17P25H03,L35P109F09	
E4922	G313			351.309	1198.38	3.441 L24P9D03,L35P119E06	
E717	3860163 (AF098962) disease resistance protein RRP1-WsA...+;			2390.599	8152.61	3.411 J127F12F1	
E3584	4263698 (AC006223) unknown protein [Arabidopsis thaliana] +2			3183.819	10836.92	3.41 L18P15E01,L35P87G02	
E1067	4263712 (AC006223) putative ribosomal protein S12 [Ara... +3	:		1747.757	5921.72	3.404 L16P6F09,L35P105H10	
E6869				1054.3	3566.42	3.388 L17P3D05,L35P111B02	
E1820	510730 (L27087) nitrate reductase [Artificial gene]	+2	232	€	1176.499	3970.87	3.383 J47G05F1
E1559	2244869 (Z97337) hypothetical protein [Arabidopsis tha... +2	35		514.614	1728.79	3.375 L28P1D08,L35P119F02	
E4575	G1275			245.182	823.45	3.359 L20P2E02,L35P116B11	
E3692	4510363 (AC007017) putative DNA-binding protein [Arabi... +3	:		1717.776	5752.91	3.359 J123F05F1	
E76	4678328 (AL049658) aldehyde dehydrogenase (NAD+-like ... +2			2872.597	9619.28	3.349 L17P14G05,L35P107B05	
E4364	G43			1187.96	3978	3.349 L16P7G07,L35P80D07	
E4003	isocitrate dehydrogenase			530.574	1775.13	3.349 J121A05F1	
E1507	132939 60S RIBOSOMAL PROTEIN L3 >pir JQ0771 ribosoma.			1524.216	5097.01	3.346 L15P4E04F1	
E3717				2832.274	9469.4	3.344 L20P1E03,L35P116B01	
E2251				1323.509	4421.93	3.343 L17P17F02,L35P107H06	
E3730				2326.41	7772.23	3.341 L22P1C08,L35P93F07	
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 cal			1459.493	4873.94	3.341 L17P15G10,L35P107C07	
E346				878.49	2914.07	3.339 L17P41E07,L35P111D01	
E3420	4689436 (AF143096) peptidyl-prolyl cis-trans isomerase... +3	2:		1614.557	5355.69	3.317 L17P20G03,L35P83A08	
E809	3193289 (AF069298) similar to several small proteins (... +3	13:		864.805	2864.04	3.317 L15P9E08,L35P103D02	
E4325	G533			1409.002	4662.43	3.312 L18P27E05,L35P88F05	
E766				697.82	2307.46	3.309 J121D09F1	
E1663	4454019 (AL035396) SRG1-like protein(dioxygenase- ethylene			569.244	1881.89	3.307 L18P17B01,L35P87G10	
E3735	3421123 (AF043538) 20S proteasome beta subunit PBG1 [A... +			1704.525	5632.2	3.306 L22P1C08,L35P117D07	
E3934	3204125 (AJ006766) putative Pi starvation-induced prot... +3	3:		400.358	1318.75	3.304 L17P16A07,L35P107C12	
E3296	2781394 (U70424) O-methyltransferase 1 [Arabidopsis th... +3	:		1474.695	4854.49	3.294 L17P27G08,L35P109H09	
E1099	3298540 (AC004681) unknown protein [Arabidopsis thaliana] +1			669.604	2202.89	3.292 L34P4G06,L35P120D08	
E2857	4455210 (AL035440) putative aspartate-tRNA ligase [Ara... +3	:		813.021	2670.01	3.29 L17P6H07,L35P111H04	
E1665	3790587 (AF079182)(Ring finger not in Tgene) RING-H2 finger			2269.208	7443.96	3.284 L16P5D02,L35P79G01	
E670	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2			1471.898	4827.59	3.28 L22P1D05,L35P117D09	
E4057	glutamate--ammonia ligase			741.002	2427.19	3.276 L20P2E04F1	
E3388	4490705 (AL035680) ribosomal protein L14-like protein ... +1	{		921.759	3014.99	3.271 L15P7G03,L35P102F09	
E3689				2780.863	9067.83	3.261 L17P14E11,L35P107B02	
E4921	G512			275.648	897.92	3.257 J127F04F1	

E719	3128217 (AC004077) hypothetical protein [Arabidopsis thaliana] +1	7	1158.737	3769.54
E3161	99772 ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana	+1	742	870.311
E4444	G371			2826.04
E2090	2827714 (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]	+1	19	788.273
E4635	G209			2557.23
E3772	4415907 (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] +1		3951.993	12816.77
E1417	3212854 (AC004005) unknown protein [Arabidopsis thaliana] +1		532.489	1725.01
E3228	3395756 (U76297) plantacyanin [Arabidopsis thaliana] > ... +1	5:	1596.285	5159.14
E3722			3668.962	11803.09
E854	3395756 (U76297) plantacyanin [Arabidopsis thaliana] > ... +1	5:	1760.945	5648.46
E1289	2281631 (AF003096) AP2 domain containing protein RAP2.... +1		1305.348	4180.1
E3807	1076364 pathogen-inducible protein CXC750 precursor - ... +1	4	2186.585	6986.49
E1463	2062164 (AC001645) jasmonate inducible protein isolog ... +2	2:	5930.997	18923.79
E1619	2497953 MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN 1		1772.878	5653.96
E1155	4531445 (AC006224) unknown protein [Arabidopsis thaliana] +3		806.495	2565.48
E3697	2132017 (Ring finger not in Tfgene) hypothetical protein YOL132C		636.055	2018.59
E2690	3335363 (AC003028) hypothetical protein [Arabidopsis thaliana] t... +1	4:	1358.499	4308.42
E1307	3702317 (AC005397) unknown protein [Arabidopsis thaliana] ... +2		1173.118	3708.95
E2911	2244798 (Z97336) hypothetical protein [Arabidopsis thaliana] ... +3	62	1429.785	4518.98
E673	4415940 (AC006418) hypothetical protein [Arabidopsis thaliana] ... +2	3:	1706.837	5389.83
E4908	G207		1800.535	5683.14
E2048			185.282	583.94
E845			478.257	1505.45
E4983	G1237		1821.976	5725.94
E4664	G553		969.652	3046.05
E2742			1121.248	3516.02
E3131			349.022	1092.1
E2864			1719.006	5375.91
E2548	4753652 (AL049751) short-chain alcohol dehydrogenase I... +3		1254.037	3903.64
E2907	4581173 (AC006220) putative glycine-rich protein [Arabidopsis thaliana] +2	6:	2816.724	8750.07
E3227	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2		2297.25	7128.69
E1603			623.302	1929.42
E529			917.657	2828.78
E1847	G899		1611.586	4954.47
E1532			1718.845	5280.74
E3527	2244904 (Z97339) similar to hypothetical protein C02F5... +1	3(490.786	1506.01
E4758	G899		1675.775	5139.19
			415.821	1274.46

E3857	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f...	302.534	926.45	3.062 L17P22D08,L35P109C04	
E748	2245108 (Z97343) EREBP-4 homolog [Arabidopsis thaliana] +3	416.392	1274.27	3.06 L18P10D06,L35P87D10	
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER	1794.692	5491.37	3.06 L17P17F09F1	
E1840	1171991 PHENYLALANINE AMMONIA-LYASE 1 >pir S52990 p	1084.554	3315.95	3.057 L23P8E04,L35P119A10	
E2126	G348	3171.053	9680.43	3.053 L20P17D07,L35P92A08	
E3468	G654	1263.584	3849.59	3.047 L15P9G04,L35P103D08	
E3467	2570507 (AF022736) ribosomal protein [Oryza sativa]	+2 4 ^c	2305.627	7007.73	3.039 L15P9G03,L35P103D07
E2100	4371290 (AC006260) unknown protein [Arabidopsis thaliana] +3	3297.989	10018.34	3.038 L20P2A12,L35P92D06	
E3176	4115925 (AF118222) contains similarity to RNA recognit... +3 4.	3331.189	10105.85	3.034 L15P4D11,L35P101F02	
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME)	3169.81	9614.02	3.033 L18P7C03,L35P115A12	
E1421	2253010 (Y14199) MAP3K delta-1 protein kinase [Arabido... +2	909.925	2759.05	3.032 L18P9G03,L35P115C05	
E4067	Actin2	1700.001	5152.09	3.031 L33P3E02F1	
E1425	1657621 (U72505) G6p [Arabidopsis thaliana] >gi 306871... +3	1699.504	5147.83	3.029 L20P11E05,L35P115D03	
E3724	1709446 PYRUVATE DEHYDROGENASE E1 COMPONENT, Al	2022.099	6118.54	3.026 L17P15B11,L35P107B07	
E568	2244816 (Z97336) hypothetical protein [Arabidopsis tha... +2 3 ^c	236.12	714.07	3.024 L17P39B01,L35P85F09	
E535	3805847 (AL031986) putative protein [Arabidopsis thaliana] +1 2	2402.209	7259.04	3.022 L17P3C04,L35P85H06	
E3886	2642215 (AF030386) NOI protein [Arabidopsis thaliana]	2053.877	3184.1	3.021 L17P27C06,L35P109H03	
E3416	E3416	2568.982	7746.71	3.015 L15P9B06,L35P103C04	
E2420	E2420	1395.69	4204.52	3.013 L22P3A12,L35P95D12	
E4340	G1045	202.41	607.62	3.002 J121F01F1	
E3406	400515 NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT	1498.349	4496.92	3.001 L15P8F02,L35P103A06	
E3285	3805847 (AL031986) putative protein [Arabidopsis thali... +1 2 ^c	882.927	2649.39	3.001 L34P1D11,L35P120B09	
E953	3250675 (AL024486) putative protein [Arabidopsis thali... +3 17.	2101.751	6298.87	2.997 L18P33B03,L35P89F11	
E564	E564	1128.929	3383.02	2.997 J27D01F1	
E3188	99697 glutamate--ammonia ligase (EC 6.3.1.2), cytoso... +2 3 ^c	4552.125	13639	2.996 L15P4H11,L35P101H02	
E2110	2781362 (AC003113) F24O1.18 [Arabidopsis thaliana]	+2 5	1437.193	4299.38	
E3178	3811007 (AB019327) NADP specific isocitrate dehydrogen... +2	4356.614	12977.44	2.992 L20P2H05,L35P92F04	
E3443	2529229 (AB007907) 6-phosphogluconate dehydrogenase [G... :]	2031.72	6044.5	2.979 L15P4E04,L35P101F04	
E536	465820 HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHRC	2104.883	6257.66	2.975 L16P11B01,L35P103H01	
E4353	G941	1220.253	3626.06	2.973 L17P30F01,L35P85A07	
E3828	E3828	3540.908	10517.83	2.972 J121G11F1	
E4011	gst6	453.832	1348.04	2.97 L17P1F11,L35P108F08	
E1480	137465 VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE	598.703	1771.63	2.959 L20P14C03,L35P115E10	
E1490	E1490	1304.652	3854.67	2.955 L20P16E04,L35P115G08	
E1577	1755178 (U75200) germin-like protein [Arabidopsis thal... +1 4 ^c	1932.056	5706.99	2.954 L20P9C08,L35P116E11	
E3448	1755156 (U75189) germin-like protein [Arabidopsis thal... +1 36	3780.894	11130.29	2.944 L16P11D06,L35P103H06	
E3858	G398	624.147	1837.36	2.944 L17P22E01,L35P109C05	

E2854	946.209	2783.86
E2916	983.61	2888.54
E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana]	+3 49
E3838	3860261 (AC005824) putative acidic ribosomal protein [... +1	34
E4638	G233	5806.561
E3481	1710530 60S RIBOSOMAL PROTEIN L27A >pir S71256 riboso.	3085.137
E4007	CYSTEINE PROTEINASE 2 PRECURSOR	712.487
E2487	3915085 TRANS-CINNAMATE 4-MONOXYGENASE (CINNAM	982.144
E3702	3297815 (AL031032) putative protein [Arabidopsis thali... +1 21:	1310.992
E1482		511.084
E3549	2160158 (AC000132) Similar to elongation factor 1-gamm... +3	4501.635
E598	4678953 (AL049711) hypothetical protein fragment [Arab... ... +1 ξ	680.915
E4053	endochitinase	479.972
E3137	3915824 [Segment 2 of 2] 60S RIBOSOMAL PROTEIN L5	3074.236
E3575	2052379 (U66343) calreticulin [Arabidopsis thaliana]	+3 126
E1193	1169383 DNAJ PROTEIN HOMOLOG AT J >gi 5355588 (L36113)	989.204
E4524	G1093	641.649
E1218	4559385 (AC006526) putative cyclic nucleotide-regulate... +1 6:	1994.48
E2791	461729 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN G	1168.569
E1825	872030 (X88774) aspartic protease [Brassica oleracea]	+2 1{
E1473	4204263 (AC005223) 40409 [Arabidopsis thaliana]	+3 36.
E612		749.293
E2800		623.439
E4549	G1390	497.709
E2790	1362162 beta-glucosidase BGQ60 precursor - barley >gi ... +2	159.539
E3540	399013 ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/A	2489.43
E1616	4510370 (AC007017) unknown protein [Arabidopsis thaliana] +1	3505.42
E702		1090.807
E1827	3510254 (AC005310) putative zinc transporter [Arabidop... +3 3	1175.38
E1957		816.439
E1595	2506276 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUB	1226.194
E3531	3168840 (U88711) copper homeostasis factor [Arabidopsi... +1	1384.018
E2607		2531.493
E4391	G1039	893.754
E1437		7123.13
E4563		2514.19
E1448		431.035
		1210.14
		898.738
		2522.5
		255.486
		716.56
		1005.686
		2816.55

E1527	3128183 (AC004521) unknown protein [Arabidopsis thaliana] +2	907.775	2538.13	2.796 L20P7D01,L35P116E03	
E3936		839.721	2338.04	2.784 L17P27G11,L35P109H11	
E6736	3851530 (AF065435) nodulin [Glycine max]	+2	408	2.782 J46B06F1	
E4844	G1006	1305.547	1847.63	2.779 J126E09F1	
E747		2233.173	3628.05	2.778 L18P10C02,L35P87D09	
E3546	4314378 (AC006232) putative lipase [Arabidopsis thaliana] +1	1867.57	5176.78	2.772 L16P2H03,L35P105B05	
E3490	2146733 GAST1 protein homolog (GA reg gene)(clone GASA1)	1360.823	3767.92	2.769 L16P10H12,L35P103G12	
E3726	3249099 (AC003114) EST gb T21244 comes from this gene....+	891.231	2466.9	2.768 L17P15D01,L35P107B09	
E1230	2058282 (X97377) atranbp1a(bind GTPbinding proteins - cell	1078.886	2983.74	2.766 L18P25D09,L35P113C04	
E2887	2914704 (AC003974) unknown protein [Arabidopsis thaliana] +1	1510.841	4170.37	2.76 L16P2E05,L35P79D07	
E1348	3021270 (AL022347) serine/threonine kinase -like prote...+3	1454.956	4008.92	2.755 L18P4H10,L35P114G03	
E4699	G735	178.122	489.19	2.746 J125C01F1	
E1264	2347098 (U76845) ubiquitin-specific protease [Arabidop...+2	62	681.039	2.738 L18P1G02,L35P113A08	
E673	4415940 (AC006418) hypothetical protein [Arabidopsis t...+2	3:	3398.112	2.734 L17P7B12,L35P86G12	
E4003	isocitrate dehydrogenase	493.061	1347.51	2.733 L15P4E04F1	
E1410	3426062 (AJ007587) monooxygenase [Arabidopsis thaliana] +2	1716.085	4685.91	2.731 L18P6E11,L35P115A06	
E1444	3451072 (AL031326) putative protein [Arabidopsis thali...+3	46.	1672.133	2.727 L20P15G08,L35P115G04	
E1081	2970654 (AF052058) ferritin subunit cowpea2 precursor ...+3	4	420.556	2.726 L17P41G03,L35P111D06	
E3424	730456 40S RIBOSOMAL PROTEIN S19	+3	42	2352.986	2.724 L15P9F09,L35P103D06
E3488	4567232 (AC007119) putative 40S ribosomal protein S25 ...+2		3590.379	2.722 L16P10H07,L35P103G10	
E5133	G322	577.411	1569.34	2.718 J129B05F1	
E4407	G353	866.458	2354.51	2.717 J122D01F1	
E2378		2543.14	6904.62	2.715 L22P3E03,L35P95E01	
E5338		320.333	869.49	2.714 J56G06F1	
E3564	1706958 (U58284) cellulose synthase [Gossypium hirsutum] +1	518.144	1406.26	2.714 L16P6E06,L35P105H05	
E6574		1074.685	2911.7	2.709 J44F02F1	
E4305	G277	1017.196	2754.86	2.708 J121A11F1	
E2132		2149.457	5819.23	2.707 L20P1B11,L35P92B08	
E3428	3164140 (D78605) cytochrome P450 monooxygenase [Arabid...+	1290.333	3489.23	2.704 L16P10A04,L35P103E04	
E3723	3135264 (AC003058) unknown protein [Arabidopsis thaliana] +3	835.184	2257.03	2.702 L17P14E05,L35P107A12	
E1821		1017.395	2740.28	2.693 L28P1D11,L35P119F03	
E2765	4467147 (AL035540) putative protein [Arabidopsis thali...+1	24.	2205.206	2.692 L24P1C02,L35P97G02	
E832	1717952 UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SI	2177.598	5858.84	2.691 L18P23C05,L35P88B10	
E2023	4371290 (AC006260) unknown protein [Arabidopsis thaliana] +2	2266.386	6092.06	2.688 L20P15H06,L35P91H01	
E2308		1950.366	5238.59	2.686 L22P21D05,L35P94G04	
E2266		2112.627	5664.69	2.681 L22P13G01,L35P93H10	
E3712	1350956 40S RIBOSOMAL PROTEIN S20 (S22)	+2	2071.695	2.68 L17P17B07,L35P107G06	

E2904	3096947 (Y16327) putative cyclic nucleotide-regulated ... +3	29:	2032.429	5445.27
E3879	3122673 60S RIBOSOMAL PROTEIN L15 >emb CAB10447 (Zc		1519.455	4064.16
E3751			2627.801	7024.33
E2753			1120.875	2995.42
E6564	464621 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >pir S28..		686.857	1833.65
E256	1903360 (AC000104) Similar to Arabidopsis 2A6 (gb X830... + 1		2086.524	5568.25
E2423			2174.23	5802.16
E3412			751.232	2001.82
E4707	G911		193.038	513.68
E4470	G1351		829.267	2205.63
E3861			511.979	1359.81
E3287			1726.464	4578.97
E3854	480450 ketol-acid reductoisomerase (EC 1.1.1.86) - Ar... +3	59	1481.27	3912.48
E2099			1188.879	3138.16
E3719			1920.981	5051.66
E3418			1972.392	5184.41
E3426	2864622 (AL021811) putative protein [Arabidopsis thali... +1	34:	4130.401	10856.46
E2380	4539459 (AL049500) putative protein [Arabidopsis thali... +1	19:	1693.624	4449.13
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana] +2	7:	4274.477	11223.26
E3862			1473.501	3864.24
E3880	3702327 (AC005397) unknown protein [Arabidopsis thaliana] +2		2417.112	6336.64
E711			646.472	1693.56
E3598	4678921 (AL049711) putative calmodulin [Arabidopsis th... +1	5	3605.817	9443.29
E4633	G508		1738.583	4544.03
E716	3309082 (AF076251) calcineurin B-like protein 1 [Arabi...	+3	473.819	1238.14
E2892			4196.404	10964.88
E2203	G483		578.79	1511.63
E1854			1637.478	4268.05
E2856			1777.328	4632.29
E715	G1334		515.459	1343.15
E3263	1806140 (X97314) cdc2MsC [Medicago sativa]	+3	1475.378	3844.44
E4471	G284		975.867	2542.47
E3116	1532169 (U63815) similar to a E. coli hypothetical pro... +1	240	924.667	2408.79
E5140	G411		2882.292	7494.38
E5312			343.627	892.57
E5465	4587529 (AC007060) Strong similarity to F1913.2 gi 303... +1	3c	329.656	856.15
E2754	2980766 (AL022198) putative calmodulin-binding protein... +2	4	1149.054	2984.06

E4053	endochitinase		402.21	1042.29
E2018			1471.6	3813.27
E3737	3687235 (AC005169) putative copia-like transposable element	+1 5	2404.197	6226.42
E784	3420008 (AF000307) steroid sulfotransferase 3 [Brassicaceae]	+1 2	2963.075	7671.23
E2257			1202.714	3112.11
E4416	G776		474.987	1228.24
E528	3329368 (AF031244) nodulin-like protein [Arabidopsis thaliana]	+3 44	1069.626	2765.63
E1134	445612 ribosomal protein S19 [Solanum tuberosum]	+2 31	1495.627	3848.45
E1874			876.538	2255.41
E4739	G1029		530.102	1358.63
E4069	caffaic o-methyltransferase		561.6	1438.48
E754			616.49	1577.41
E1597	419757 ketol-acid reductoisomerase (EC 1.1.1.86) precursors	+1 2	2092.316	5350.57
E2238			3299.219	8418.19
E3714	484656 monodehydroascorbate reductase (NADH) (EC 1.6....+)		4129.406	10536.21
E3191	3023858 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT		1779.578	4538.78
E5157			268.749	685.31
E1811			1415.702	3606.26
E3343	4753651 (AL049751) ribosomal protein L13a like protein...+2 5		3606.265	9185.06
E1459	2281112 (AC002333) endochitinase isolog [Arabidopsis thaliana]	+1 1	678.106	1725.3
E1610	3786008 (AC005499) unknown protein [Arabidopsis thaliana]	+2	953.294	2420.03
E6399	2633544 (Z99110) ycl1 [Bacillus subtilis]	+3 198 1.8e	634.017	1607.69
E3189	2129570 DAD-1 homolog - Arabidopsis thaliana >emb CAA6...+:		2181.924	5526.96
E4518	G1050		463.428	1173.38
E3181	3395427 (AC004683) unknown protein [Arabidopsis thaliana]	+2	1499.406	3793.28
E2426	3023522 COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN)		1005.363	2541.11
E2209			1431.438	3613.57
E4314	G321		1096.835	2766.48
E2629			2178.208	5492.76
E1442	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ...+:		3511.188	8846.47
E2010	3157937 (AC002131) identical to aspartic proteinase ccd...+3 1		5679.911	14308.81
E1015	2493052 ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL		2206.113	5557.42
E2058			402.719	1014.18
E0	NULL		623.812	1570.11
E744	3915710 G-BOX BINDING FACTOR 1 >emb CAA68197 (X9994		272.341	685.09
E761	3395441 (AC004683) unknown protein [Arabidopsis thaliana] +1		1720.05	4321.36
E200	1402900 (X98322) peroxidase [Arabidopsis thaliana] >em...+3		562.321	1412.4

E5503	2708749 (AC003952) putative senescence-assoc. rhodanes...+2	216	989.448	333.29	2.969	3	3
E6511	3033375 (AC004238) putative berberine bridge enzyme [A...+3	285	: 1592.617	536.91	2.966	1	5
E2531	3461828 (AC004138) unknown protein [Arabidopsis thaliana] +1	158	1901.73	641.75	2.963	1	8
E1112	2245066 (Z97342) Beta-Amylase [Arabidopsis thaliana]	+2	360 3..	9207.632	3110.64	2	16
E2266				1933.051	653.46	3	12
E4693	G713			1065.144	361.56	2.958	3
E5554	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NAD			1371.105	465.6	2.946	3
E1458	499301 (X77116) ABI1 [Arabidopsis thaliana] >gi 54998...+1	351 1..	11733.7	3996.48	2.936	2	2
E1308	1170034 GLUTAMATE-CYSTEINE LIGASE PRECURSOR (GAMMA-			13616.3	4638.57	2.935	4
E5632	2894563 (AL021890) putative protein [Arabidopsis thali...+1	293 2..7	3204.744	1100.29	2.913	1	3
E1220	E5509 3549656 (AL031394) putative protein [Arabidopsis thali...+2	636 1..4	1931.032	664.54	2.906	3	17
E5373	1169544 ERD1 PROTEIN PRECURSOR >pir JN0901 ERD1 prote...+			9629.566	3335.98	2.887	3
E1027	E1868 4678332 (AL049658) putative peptide transporter [Arabi...+3	311 3..2	7595.683	2644.26	2.882	1	16
E5386	99698 glutamate-ammonia ligase (EC 6.3.1.2), cytoso...+2	966 1..5	877.809	306.08	2.868	1	19
E5448	4105633 (AF048982) putative ethylene receptor [Arabido...+3	902 1..	896.904	312.97	2.866	1	2
E5802	2642446 (AC002391) similar to auxin-responsive GH3 pro...+1	225 ..	23772.087	830.55	2.856	1	3
E5608	E3696 4581500 (AL034352) putative oxalyl-CoA decarboxylase [...] +1	93 7..	1713.956	600.81	2.853	2	2
E5095	G515 629602 probable imbibition protein - wild cabbage >em...+3	514 3..8	2668.509	935.77	2.852	1	15
E2706	E5960 2924517 (AL0222023) putative protein [Arabidopsis thali...+3	379 1..8	2221.861	780.94	2.846	3	22
E4050	E4777 pathogen-inducible protein CXc750			2500.776	879.76	2.845	3
E1477	E2706 1170034 GLUTAMATE-CYSTEINE LIGASE PRECURSOR (GAMMA-			4767.409	1680.95	2.836	1
E6038	E3325 G350			16428.07	5792.45	2.836	1
E5067	E2396 E3686 1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go...+2	231 5..2	4839.303	927.84	2.831	2	3
E2343	E2343 4469007 (AL035602) UDP rhamnose-anthocyanidin-3-glucos...+2	67	4349.538	940.4	2.824	1	14
E6633	E6633 541849 anthranilate synthase (EC 4.1.3.27) beta chain...+3	367 1..9	5652.704	1721.56	2.812	1	21
E4006	E3313 3341680 (AC003672) unknown protein [Arabidopsis thaliana] +3	293	1163.712	1547.9	2.811	1	12
E4731	E464367 VACUOLAR ATP SYNTHASE			704.238	2019.47	2.799	1
E605	E605 4689366 (AF134155) RING finger protein [Arabidopsis th...+3	294 3..	7891.665	252.33	2.791	1	15
E2355	E2355 2894607 (AL021889) NAM (no apical meristem) - like pro...+1	186 3..	3935.766	592.34	2.788	1	12
				608.948	218.8	2.783	1
					2835.92	2.783	1
					1414.77	2.782	1

E6058	2959736 (Y13651) homologous to GATA-binding transcript...+3	148	651.211	234.43	2.778	3	2
E5378	2500981 GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--T RNA LIG)	1263.362	455.1	2.776	2	1	2
E4218		2364.246	852	2.775	3	2	22
E6104	4417286 (AC007019) putative shikimate kinase [Arabidop...+3	345.1	781.675	282.47	2.767	2	3
E648	1946361 (U93215) C3HC4 zinc finger protein isolog [Ara...+1	973.3!	328.689	118.88	2.765	1	2
E6933	3522935 (AC004411) putative alcohol dehydrogenase [Ara...+1	589	350.024	126.6	2.765	1	10
E5280	4337198 (AC006403) putative auxin-induced protein [Ara...+1	905.5	584.691	211.49	2.765	2	7
E3204	3763924 (AC004450) putative extensin [Arabidopsis thal...+3	270.1:	1575.803	570.12	2.764	3	14
E5465	4587529 (AC007060) Strong similarity to F1913.2 gj 303...+1	338.6.0	1459.146	528.91	2.759	1	2
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t...+1	125.3!	5219.338	1896.14	2.753	3	8
E4569	G1308		713.836	259.89	2.747	4	1
E106	4504085 glycerol-3-phosphate dehydrogenase 2 (mitochon...+2	152	2744.45	999.13	2.747	1	19
E2178		632.505	230.3	2.746	1	3	12
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 calnex...	12668.82	4629.05	2.737	4	1	16
E6813	4587607 (AC006951) putative antisense basic fibroblast...+1	524.9!	639.23	234.22	2.729	2	6
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana +3	840.2.8	2726.529	999.52	2.728	3	21
E5692	3941524 (AF062916) putative transcription factor [Arab...+3	376.3.7	996.258	365.73	2.724	2	2
E4005	3' flavonoid O-methyltransferase	3136.753	1152.17	2.722	1	3	1
E6744		1752.881	645.43	2.716	2	3	5
E3266	1684851 (U77935) Dnaj-like protein [Phaseolus vulgaris] +2	188.5.	1815.439	669.72	2.711	2	19
E6736	3851530 (AF065435) nodulin [Glycine max]	+2	408.2.6e-3	3454.805	1274.55	2.711	4
E4077	6-Human metallothionein-II gene		1718.611	636.62	2.7	2	3
E4662	G545		1377.299	510.58	2.698	4	4
E1347	2262098 (AC002343) HSP90 isolog [Arabidopsis thaliana] +3	632.2	2096.872	778.17	2.695	1	18
E2979	2191147 (AF007269) A_G002N01.26 gene product [Arabido...+1	20	3755.182	1395.52	2.691	1	20
E1229		425.247	158.13	2.689	1	1	17
E7045	2341040 (AC000104) EST gb H76414 comes from this gene...+2	44	763.188	284.15	2.686	1	6
E3518	3668173 (AB006777) vegetative storage protein [Arabido...+1	682.1.	1696.018	632.62	2.681	2	4
E5814	2342686 (AC000106) Similar to Saccharomyces hypothetic...+3	798	1232.269	459.77	2.68	3	14
E2212		626.345	233.89	2.678	1	3	12
E3248	3660471 (AJ001809) succinate dehydrogenase flavoprotei...+3	424!	5307.817	1982.47	2.677	4	18
E3530	3695019 (AF055848) subtilisin-like protease [Arabidops...+1	349.6.3	7629.209	2852.17	2.675	2	2
E5644	4185144 (AC005724) unknown protein [Arabidopsis thaliana] +2	484	1163.467	435.15	2.674	1	4
E6199		756.26	282.95	2.673	1	1	4
E5376	2213583 (AC000348) T7N9.3 [Arabidopsis thaliana] +2	138.4.3	3480.508	1303.19	2.671	1	2
E2154	3913518 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5...+3	3!	1365.225	511.35	2.67	2	11
E5132	G179		1290.881	483.58	2.669	3	1

E3005	3548819 (AC005313) putative heterogeneous nuclear ribo...+1	187	1790.125	671.77	2.665	14
E2309			2922.322	1096.51	2.665	2
E2354			2233.309	838.32	2.664	2
E4471	G284		514.03	193.11	2.662	4
E5312			4525.61	1701.27	2.66	3
E2042	2578440 (X67425) pectinesterase [Pisum sativum]	+1	147 2.6e	6018.451	2264.08	2
E2444	3123188 CATALASE 3>gi 2347178 (U43147) catalase 3	[Ar...+2	45z	9507.56	3580.43	3
E3463	VACUOLAR ATP SYNTHASE			6967.048	2634.39	3
E4006	2262105 (AC002343) unknown protein [Arabidopsis thaliana] +3	682	460.868	174.3	2.645	14
E1003	G1080		448.034	169.55	2.644	2
E4573			506.333	191.66	2.642	1
E4547	1709798 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >		1828.011	692.12	2.642	20
E5845			1421.691	539.64	2.635	1
E2410			997.137	378.84	2.632	3
E6137			1602.038	609.82	2.627	12
E7022	2529229 (AB007907) 6-phosphogluconate dehydrogenase [G...+1	5z	15221.34	5793.24	2.627	4
E3028			838.031	319.37	2.624	7
E6269	2118045 beta-fructofuranosidase (EC 3.2.1.26) - Arabid...+2	929 3.2	1913.601	729.23	2.624	3
E5368	4704730 (AF121355) peroxiredoxin TPx1 [Arabidopsis tha...+2	655 z	2157.993	822.48	2.624	4
E6973			466.259	177.9	2.621	1
E3624	3859606 (AF104919) contains similarity to cysteine pro...+1	214 2.3e	12746.54	4863.44	2.621	7
E5362	E5362 2832677 (AL021712) hypothetical protein [Arabidopsis t...+2	203 4.2	729.29	278.34	2.62	16
E4005	3' flavonoid O-methyltransferase		1312.004	501.03	2.619	2
E5858			1368.123	522.95	2.616	1
E3085			4158.376	1590.74	2.614	3
E3585	2129769 xyloglucan endo-transglycosylase precursor - A...+1	756 3.	23791.86	9108.56	2.612	13
E6373	2511546 (AF022658) putative c2h2 zinc finger transcrip...+1	351 8.4	1177.256	451.09	2.61	16
E4005	3' flavonoid O-methyltransferase		1768.03	677.96	2.608	4
E5935			1227.655	471.49	2.604	1
E2627			3054.771	1174.6	2.601	3
E5788	2642153 (AC003000) unknown protein [Arabidopsis thaliana] +3	494 2	520.807	200.31	2.6	12
E2916			8251.989	3174.27	2.6	4
E6889	4538929 (AL049483) putative nucleic acid binding prote...+1	132 8.6	1312.916	505.11	2.599	1
E1714			3910.832	1505.51	2.598	6
E4026	thionin		1040.371	400.61	2.597	18
E6525	3128184 (AC004521) unknown protein [Arabidopsis thaliana] +1	405	608.636	234.58	2.595	1

E580	541848 amino acid transport protein I - Arabidopsis t... +3 580 1.6e-10	13797.22	5335.56	2.586
E2503	510876 (X80051) NADP dependent malic enzyme [Phaseolus vulgaris] +1 16	5926.541	2292.92	2.585
E6942	2078350 (U95923) transaldolase [Solanum tuberosum] +1 330 4	2482.999	961.08	2.584
E2491		4316.73	1671.89	2.582
E5464	1699053 (U78868) putative aspartate-arginine-rich mRNA... +2 174 1	1825.392	707.88	2.579
E4279		354.645	137.63	2.577
E5354	3935145 (AC005106) T25N20.9 [Arabidopsis thaliana] +1 277 2.	573.369	222.48	2.577
E4179	Cre		2107.205	819.65
E6976	2317729 (AF013627) reversibly glycosylated polypeptide... +2 610 1.! E6976	2789.129	1085.83	2.569
E2533		2835.498	1104.34	2.568
E4565	G926	403.253	157.13	2.566
E4246	3123712 (D89051) ERD6 protein [Arabidopsis thaliana] +2 417 2.! E4246	3548.067	1384.75	2.562
E96		4805.683	1877	2.56
E2297	1778095 (U64903) putative sugar transporter; member of... +3 325 1	5458.931	2135.11	2.557
E4026	thionin	1501.763	587.6	2.556
E0	NUL	595.142	233.17	2.552
E4076	5-Human cathepsin O or X mRNA	1714.057	672.03	2.551
E875	4262242 (AC006200) NADC homolog [Arabidopsis thaliana] +2 525	3690.816	1448.71	2.548
E1607	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +2 663	3273.503	1285.46	2.547
E1562	3164138 (D788604) cytochrome p450 monooxygenase [Arabidopsis thaliana] +3 38	1206.6	473.87	2.546
E4077	6-Human metallothionein-II gene	2247.977	882.99	2.546
E6153	3892722 (AL033345) putative protein [Arabidopsis thaliana] +1 262 7.3e-05	572.516	225.2	2.542
E6247		934.655	367.76	2.541
E6026		1503.546	591.66	2.541
E1265	1703220 ALG2 PROTEIN >gi 1127806 (U40857) ALG2 [Arabidopsis thaliana] +2 5	1806.111	711.42	2.539
E6503	2894571 (AL021890) putative protein [Arabidopsis thaliana] +2 170 7.0e-05	869.63	343.76	2.53
E0	NUL	593.799	235.64	2.52
E5968	285286 flavonol 4'-sulfotransferase - Flaveria chlora... +2 218 3.4e-1	1865.821	740.46	2.52
E6792	629602 probable imbibition protein - wild cabbage >em... +3 202 2.6	3189.442	1270.93	2.51
E2290		7639.846	3044.15	2.51
E1739	1817544 (D83025) proline oxidase precursor [Arabidopsis thaliana] +1 328	955.491	381.65	2.504
E2329		2720.775	1087.98	2.501
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsis thaliana] +3 462 3..	6627.67	2649.59	2.501
E4358	G1007	555.161	222.04	2.5
E6145	4038034 (AC005936) unknown protein [Arabidopsis thaliana] +1 328	5712.592	2286.45	2.498
E4084	14-Human IgSF full-length EST	4422.226	1771.58	2.496
E5704		7218.334	2891.39	2.496

E232	9	20
E4819	G865	428.085
E6213	3021280 (AL022347) serine /threonine kinase - like pro... +1	293 6.3e
E5073	G242	601.344
E1887	4531444 (AC006224) putative protein kinase [Arabidopsi... +1	384 9.
E4014	CATALASE 3	251.4
E4050	pathogen-inducible protein CXc750	2.392
E2987	G664	601.344
E2764	2244973 (Z97340) similarity to extensin class 1 protei... +2	240 3.2e-
E2546	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3	680 123.1
E1620	3451078 (AL031326) putative protein [Arabidopsis thali... +1	250 1.1e
E6074	4128133 (AJ006068) dTDP-D-glucose 4,6-dehydratase [Hom... +2	30 4554.506
E4492	G1390	13231.576
E2029	1421741 (U54770) cytochrome P450 homolog [Lycopersicon... +1	10. 377.585
E5370	E2718	1838.15
E5712	3687688 (AF057027) response regulator protein [Brassic... +1	281 6.
E6748	3688191 (AJ010090) MAP3K alpha protein kinase [Arabido... +1	203 5804.637
E2968	3540182 (AC004122) Unknown protein [Arabidopsis thaliana] +1	407 807.799
E2273	E4075	1569.41
E5742	4-Human Gorilla beta-2-microglobulin mRNA	2.385
E4115	cystatin B	1327.83
E3905	3193309 (AF069300) No definition line found [Arabidops... +3	647 2.1
E1149	4006829 (AC005970) putative protein kinase [Arabidopsi... +3	445 3.
E3380	E5882	2188.393
E6629	2623297 (AC002409) unknown protein [Arabidopsis thalia... +3	209 3.
E612	4337011 (AF119572) zinc-binding peroxisomal integral m... +1	317 3.
E5905	E6642	1164.549
E5353	2213626 (AC000103) F21J9.18 [Arabidopsis thaliana]	497.05
E4610	E4669	4977.945
E5076	G28	2129.03
E6944	4454036 (AL035394) putative major latex protein [Arabi... +2	527 2.3
E583	4263704 (AC006223) putative sugar starvation-induced p... +1	220 2. 3305.88

E3873	3402700 (AC004261) unknown protein [Arabidopsis thaliana] +1	623	3527.764	1514.31	2.33	16	10
E501	4115383 (AC005967) receptor-like protein kinase [Arabi... +1	180	6.4	5532.785	2377.49	2.327	1
E1015	2493052 ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >dbj.	2710.298	1165.2	2.326	1	2	16
E6319	1708971 (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (1208.096	519.57	2.325	2	1	4
E1179	1709794 26S PROTEASOME REGULATORY SUBUNIT S5A (MULTI	1596.436	686.84	2.324	2	2	16
E6317	3693.232	1589.59	2.323	2	1	4	20
E4510	348.308	150.18	2.319	2	3	3	20
E6086	5361.782	2318.79	2.312	2	2	3	2
E285	352.491	152.61	2.31	1	2	9	1
E515	2708751 (AC003952) hypothetical protein [Arabidopsis t... +3	242	8.2	1528.666	661.66	2.31	10
E617	2	6114.476	2650.53	2.307	3	4	10
E4967	G262	331.419	143.85	2.304	4	1	21
E5693	2244758 (Z97335) hypothetical protein [Arabidopsis tha... +3	363	1.5	1536.211	666.79	2.304	2
E5484	4558563 (AC007138) putative NifU-like metallocluster a... +2	538	4.4	2995.213	1302.95	2.299	1
E6825	5925.147	2577.22	2.299	2	2	2	5
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana] +2	257	844.798	368.09	2.295	1	2
E6906	3894177 (AC005312) unknown protein [Arabidopsis thaliana] +2	231	417.701	182.09	2.294	1	6
E6964	3928089 (AC005770) putative osr40 [Arabidopsis thaliana] +2	477	1	3306.903	1441.83	2.294	3
E5389	2160182 (AC000132) ESTs gbl ATTTS1236,gb T43334,gb N9701... +3	3660.669	1597.13	2.292	3	3	6
E6887	915.611	401.64	2.28	1	3	6	6
E6888	G859	786.888	345.37	2.278	1	3	6
E4497	G643	358.633	157.61	2.275	2	3	19
E6967	4371292 (AC006260) unknown protein [Arabidopsis thaliana] +1	723	423.346	186.14	2.274	1	7
E6559	G1099	814.339	358.06	2.274	3	1	5
E5677	3123329 (AJ005929) squalene epoxidase homologue [Arabi... +1	369	1047.545	460.62	2.274	2	2
E5706	3776558 (AC005388) Identical to gb L14814 DNA for tiss... +1	627	1.	2032.895	894.3	2.273	2
E4903	G1493	368.316	162.09	2.272	4	1	20
E6934	1653655 (D90915) ATP-dependent Clp protease proteolyti... +3	184	2146.173	946.73	2.267	1	7
E1869	2262177 (AC002329) hypothetical protein similar to T18... +3	337	1.7	6021.645	2658.68	2.265	4
E6405	3159.067	1395.69	2.263	2	1	1	19
E4008	AtRanBP1b protein	544.963	241.01	2.261	1	1	4
E5449	3395938 (AF076924) polypyrimidine tract-binding protein... +3	318	5.5	1698.24	751.12	2.261	2
E3575	2052379 (U66343) calreticulin [Arabidopsis thaliana]	+3	126	1.5e-0	11986.21	5300.27	2.261
E14	128405 Putative NODULIN 21 (N-21) >pir S08632 nodulin-21 - so... +	1729.13	765.36	2.259	2	2	7
E2006	3367576 (AL031135) NAM / CUC2 -like protein [Arabidops... +1	447	1832.971	811.57	2.259	2	11
E5329	916.304	406.05	2.257	4	1	1	7
E2945	464863 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING.	2038.978	905.1	2.253	2	2	13

E1491	3193289 (AF069298) similar to several small proteins (...+1 415 4.7e 1787.852	18	1	1	1	3	2.252
E5738	2702277 (AC003033) putative cyclin g-associated kinase...+1 410 6. 361.793		1	1	1	2.251	
E1186	3935169 (AC004557) F17L21.12 [Arabidopsis thaliana]		1	211	7.	1755.179	780.94
E5491	2497538 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 ...		+1	211	7.	1176.234	523.57
E2285	1363482 IAA11 protein - Arabidopsis thaliana >gi 97292...+3 434 4.5 2040.626		+3	434	4.5	908.6	2.246
E7033			683.766	304.59	2.245	1	2
E5942	3044214 (AF057044) acyl-CoA oxidase [Arabidopsis thali...+1 462 5 1467.037		+1	117	1.8	1664.9	653.51
E2332	4581180 (AC006220) putative glycine-rich protein [Arab...+3 117 1.8 1664.9		+3	117	1.8	742.03	2.244
E2807			4128.102	1839.39	2.244	1	1
E4301	G9		7759.504	3461.56	2.242	2	2
E36			326.366	145.48	2.243	1	1
E5971	2462823 (AF000657) unknown protein [Arabidopsis thalia...+2 320 2 767.167		+2	320	2	342.27	2.241
E4007	CYSTEINE PROTEINASE 2 PRECURSOR		2400.949	1071.79	2.24	2	3
E4113	cystatin B		1097.699	490.48	2.238	4	3
E441	1345592 14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (...+1 ,		+1	4168.734	1863.4	2.237	2
E7018			2941.484	1315.48	2.236	1	2
E6517	2492635 ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYD		3189.958	1427.88	2.234	1	1
E774	2642159 (AC003000) putative mannose-1-phosphate guanyl...+1 281		15021.23	6723.23	2.234	4	3
E5807	4432846 (AC006283) unknown protein [Arabidopsis thaliana]+1 639		829.294	371.62	2.232	1	1
E6901	3881976 (AJ012409) hypothetical protein [Homo sapiens]		+3 548 3	569.863	255.49	2.23	1
E4243	G738		776.563	348.16	2.23	1	2
E5607	3319340 (AF077407) contains similarity to E. coli cat...+3 467 1.5e- 2792.196		-2792.196	1252.31	2.23	4	3
E1267	2190551 (AC001229) Similar to C. elegans hypothetical ...+3 309 7.{		2464.681	1105.53	2.229	1	1
E6878			1422.257	639.01	2.226	4	2
E6760	2583124 (AC002387) 5-enolpyruvylshikimate-3-phosphate ...+2 444		1815.726	815.82	2.226	2	3
E5514	4468980 (AL035605) formamidase-like protein [Arabidops...+1 508 {		1977.73	890.02	2.222	1	2
E5809	4585983 (AC005287) Unknown protein [Arabidopsis thaliana]+3 182		1006.431	453.2	2.221	1	3
E6986			1142.294	514.22	2.221	1	2
E4155	BioB		2594.798	1168.1	2.221	4	3
E385			1884.916	849.48	2.219	2	1
E5847	1532165 (U63815) similar to dehydrogenase encoded by G...+2 506		517.021	233.19	2.217	1	4
E6042			941.93	425.28	2.215	2	3
E4004	pectinesterase		4220.655	1906.98	2.213	1	2
E5817	3980254 (AJ006053) peroxisomal membrane protein [Arabi...+1 778		424.714	192.22	2.21	1	3
E202	4508078 (AC005882) 64134 [Arabidopsis thaliana]		+3 330 1.8{	3773.66	1708.4	2.209	1
E200	1402900 (X98322) peroxidase [Arabidopsis thaliana] >em...+3 248 2		1914.446	866.88	2.208	2	8
E5815	4191782 (AC005917) WD-40 repeat protein [Arabidopsis t...+3 586 {		576.275	261.15	2.207	1	3

E5282	1076331 histidine transport protein - Arabidopsis thal...	+3	1002	3.0e-	2547.153	1154.25	2.207	7	21
E4767	G7				345.546	156.61	2.206	3	21
E3452	4490309 (AL035678) peroxidase ATP17a-like protein [Ara...]	+3	548		3820.164	1731.76	2.206	2	14
E3754	2213590 (AC000348) T7N9.10 [Arabidopsis thaliana]	+2	349	8.e	3823.256	1732.84	2.206	2	15
E4887	G1219				759.8	344.7	2.204	4	1
E4891	G784				339.994	154.58	2.199	2	1
E6657	1755152 (U75187) germin-like protein [Arabidopsis thal...]	+1	829	7.9.	711.69	323.74	2.198	3	2
E1481	2829898 (AC002311) Hypothetical protein [Arabidopsis t...]	+1	228	3.	4067.911	1851.82	2.197	2	1
E5429	120667 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, C				6705.58	3052.56	2.197	3	18
E5660					860.201	392.19	2.193	2	2
E5490					1119.084	510.78	2.191	3	2
E5452					9479.94	4327.76	2.19	1	2
E4797	G1216				507.271	231.69	2.189	1	2
E2939	1628622 (U72631) flavonol synthase [Arabidopsis thalia...]	+2	229	7.2	2528.506	1155.23	2.189	3	2
E6363	1922242 (Y10084) hypothetical protein [Arabidopsis tha...]	+1	334	1.8	7960.856	3639.86	2.187	2	13
E5052	G1099				348.57	159.45	2.186	2	2
E3225	730526 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLO				826.236	378.41	2.183	3	4
E1796					508.386	233.06	2.181	1	21
E33					3395.433	1557.08	2.181	4	14
E5949					646.547	297.25	2.175	2	1
E1029					484.788	223.23	2.172	1	2
E2720					3678.919	1693.7	2.172	1	16
E4030	4-coumarate:coa ligase - like				733.633	338.01	2.17	1	8
E4006	VACUOLAR ATP SYNTHASE				6174.026	2844.98	2.17	2	1
E4586	G1427				321.618	148.49	2.166	4	1
E1999					2758.036	1274.05	2.165	4	20
E2370	4468986 (AL035605) putative protein [Arabidopsis thali...]	+3	468	1.1e	6899.581	3191.45	2.162	2	11
E5480	4530441 (AF117756) thyroid hormone receptor-associated...	+1	158		1677.852	776.94	2.16	1	12
E3685	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi...	+3	338		3304.503	1530.32	2.159	2	2
E2708	4587615 (AC006951) putative acyl-CoA synthetase [Arabi...]	+2	264	5	1153.404	534.83	2.157	1	15
E274	3941480 (AF062894) putative transcription factor [Arab...]	-1	157	2.7e	487.331	226.28	2.154	1	8
E1077	1346387 KNOTTED-LIKE HOMEBOX PROTEIN 3 >emb [CAA63130				6326.609	2936.83	2.154	2	9
E2222					1540.824	715.68	2.153	1	2
E2670					4356.137	2022.91	2.153	1	3
E6346	3763930 (AC004450) unknown protein [Arabidopsis thaliana]	+1	613		1377.704	640.13	2.152	2	4
E6394					1367.16	635.53	2.151	2	5
E1438					1819.308	845.61	2.151	4	3

E5570	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	212	1.5e-2	699.507	325.36	2.15	2	1
E4014	CATALASE 3				7443.877	3463.97	2.149	2	1
E5789	4585983 (AC005287) Unknown protein [Arabidopsis thaliana] +3	399	1530.296	712.31	2.148	1	1	4	
E265	99725 glycine-rich protein PUTG1 - Arabidopsis thali... +3	504	1.7e-1	323.029	150.55	2.146	1	4	9
E4852	G1278				962.419	448.56	2.146	3	2
E2348	2702281 (AC003033) putative protein disulfide isomeras...	+2	732	1.4	1187.843	553.58	2.146	3	4
E4053	endochitinase				1095.189	510.61	2.145	1	4
E5453	4262186 (AC005508) Highly similar to cullin 3 [Arabido... +3	740	1.7e-1	2019.824	943.03	2.142	1	2	2
E5371	4455349 (AL035524) putative protein [Arabidopsis thali... +1	272	6.7e-1	2793.447	1305.45	2.14	1	3	2
E1335					422.408	197.63	2.137	1	4
E216	4584520 (AL049607) enoyl-CoA hydratase-like protein [A...+2	410	1.	1355.736	634.35	2.137	1	2	8
E4083	13-Human lysosomal acid lipase/cholesterol esterase				3574.403	1672.7	2.137	2	4
E4789	Maybe G881, Bad Sequence				395.86	185.36	2.136	1	2
E0	NUL				496.912	232.76	2.135	3	2
E6303	4468805 (AL035601) auxin-responsive GH3-like protein [...+1	964	3.	1979.15	927.01	2.135	3	4	5
E1691	4455287 (AL035527) putative protein [Arabidopsis thali... +1	239	1.5e-1	914.85	428.89	2.133	3	1	19
E2820					648.076	304.38	2.129	3	14
E1432	4185513 (AF102823) actin depolymerizing factor 5 [Arab...+3	595	1.	3788.252	1781.77	2.126	2	3	17
E5184	3152614 (AC004482) unknown protein [Arabidopsis thaliana] +2	734	1680.953	790.94	2.125	2	2	2	7
E2328	3193324 (AF069299) contains similarity to WD domains, ...+1	523	6.	2321.4	1092.56	2.125	1	4	12
E5919	2062157 (AC001645) jasmonate inducible protein isolog ...+2	321	1.	966.162	455.04	2.123	1	2	4
E6385	4455246 (AL035523) putative protein [Arabidopsis thali... +2	694	1.3e-1	3677.398	1733.36	2.122	4	1	4
E6068					2065.213	973.81	2.121	4	3
E4349	G921				854.439	403.05	2.12	1	1
E6595	3399769 (U76299) uolacyanin II [Arabidopsis thaliana]	+3	645	3.5e-1	1030.934	486.35	2.12	3	1
E1256	15223800 (Y07694) MAP kinase kinase alpha protein kinas...	+1	181	1	2115.815	998.17	2.12	1	3
E6000	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi...+1	880	2371.732	1120.26	2.117	2	3	3	3
E5737	2129570 DAD-1 homolog - Arabidopsis thaliana >emb CAA6...+1	34(941.018	444.76	2.116	1	1	1	3
E2093					1911.168	903.61	2.115	2	11
E2255	3292829 (AL031018) putative protein [Arabidopsis thali... +3	172	8.3e-2	1965.859	930.13	2.114	3	1	12
E646					3812.053	1804.57	2.112	1	2
E2429	4512664 (AC006931) putative ribose phosphate pyrophosp...	+2	193	3133.306	1485.96	2.109	4	1	12
E5456					2252.928	1068.87	2.108	3	2
E5512					2613.674	1239.66	2.108	1	2
E2752	1362162 beta-glucosidase BGQ60 precursor - barley >gil...+3	224	2.	442.17	209.82	2.107	1	1	13
E1744	3080402 (AL022603) putative NADPH quinone oxidoreducta...+2	65(2788.994	1323.93	2.107	1	1	4	18
E6287	3355480 (AC004218) Medicago nodulin N21-like protein [...+1	130	5	1012.354	480.7	2.106	3	4	4

E4689	G664	585960 PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT >	1697.311	827.05	2.052	20	16
E968	5862169 (AC001645) ABC transporter (PDR5-like) isolog ... +1	237	1060.928	517.78	2.049	4	4
E5917	2062169 (AC001645) ABC transporter (PDR5-like) isolog ... +1	237	2201.92	1074.48	2.049	1	2
E6539	3860258 (AC005824) unknown protein [Arabidopsis thaliana] +2	377	437.008	213.4	2.048	1	5
E6277	2829133 (AF043351) adenosine-5'-phosphosulfate kinase ... +3	983	4627.059	2259.86	2.047	1	2
E2214	4455293 (AL035528) putative protein [Arabidopsis thaliana] +1	279	1.2 ^c	447.485	218.67	2.046	4
E3902	3858935 (AL021636) synaptobrevin-like protein [Arabidopsis thaliana] +1	625	2.1	630.528	308.15	2.046	12
E581			2974.149	1454.4	2.045	1	16
E5463			1160.147	567.76	2.043	3	3
E238	Empty pMern20 vector 100 ng	G907	6595.377	3227.91	2.043	2	9
E4092			855.808	419.07	2.042	4	1
E4389			359.63	176.24	2.041	1	2
E2541			5904.514	2892.92	2.041	2	20
E4303	G192		422.805	207.24	2.04	1	11
E4405	G427		668.354	327.56	2.04	3	19
E6726			1184.269	580.57	2.04	2	19
E4050	pathogen-inducible protein CXc750		1754.469	859.89	2.04	2	1
E4227			359.106	176.12	2.039	3	5
E4694	G728		440.801	216.3	2.038	4	22
E0	NUL		620.549	304.54	2.038	3	20
E6788	2911057 (AL021961) caffeoyl-CoA O-methyltransferase - ... +2	516	2353.727	1155.76	2.037	4	3
E3426	2864622 (AL021811) putative protein [Arabidopsis thaliana] +1	342	4.8 ^c	9064.79	4450.2	2.037	6
E3066	4185139 (AC005724) putative diacylglycerol kinase [Arabidopsis thaliana] +1	499	5. ^c	1491.582	733.01	2.035	14
E6742	3378056 (AF017777) helicase [Drosophila melanogaster]	+2	138	7	917.182	451.07	2.033
E5396	4510345 (AC006921) unknown protein [Arabidopsis thaliana] +3	534	2905.466	1430.82	2.031	1	5
E6441	114815 IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B AN. G176		983.652	484.82	2.029	3	2
E2262			1057.084	520.94	2.029	2	4
E5408			821.445	405.54	2.026	1	12
E6886			941.178	464.46	2.026	1	3
E5944	3241945 (AC004625) unknown protein [Arabidopsis thaliana] +1	430	1905.203	941.08	2.024	1	6
E2046			1161.693	574.11	2.023	2	3
E5895			1900.649	939.83	2.022	1	11
E2010	3157937 (AC002131) Identical to aspartic proteinase cD... +3	118	1. ^c	1648.787	815.64	2.021	2
E3466			20921.95	10359.6	2.02	3	14
E0	NUL		384.547	190.65	2.017	4	22
E4032	ACYL CARRIER PROTEIN		784.04	388.65	2.017	1	1
E6285			1625.991	806.61	2.016	3	2

E2977	3341679 (AC003672) dynamin-like protein phragmoplastin... +1 269	1837.035	912.39	2.013	13	9
E536	465820 HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMO... +1 269	1837.035	1292.37	2.013	1	1
E6922	3643607 (AC005395) unknown protein [Arabidopsis thaliana] +2 342	881.654	438.13	2.012	1	7
E4884	4557647 heat shock factor binding protein 1 >gi 328340... +1 166 1.1	1617.72	804.37	2.011	4	1
E6333	G1552	1453.671	724.01	2.008	2	1
E4743	4468807 (AL035601) cytochrome P450 monooxygenase-like ... +2 75	5011.505	2495.75	2.008	3	1
E3359	4335749 (AC006284) unknown protein [Arabidopsis thaliana] +3 327	2 6090.818	3032.59	2.008	4	14
E617	17559.94	8747.12	2.008	4	3	16
E28	642.297	320.04	2.007	1	2	7
E6170	2832679 (AL021712) putative protein [Arabidopsis thali... +3 276 1.7e	1103.394	549.7	2.007	1	1
E5768	4262250 (AC006200) putative aldolase [Arabidopsis thali... +3 112 4e	3310.079	1649.37	2.007	2	3
E3114	4006826 (AC005970) unknown protein [Arabidopsis thaliana] +2 288	1254.524	625.48	2.006	4	1
E6453	4335749 (AC006284) unknown protein [Arabidopsis thaliana] +3 327	1511.049	753.37	2.006	2	2
E484	1310.424	653.83	2.006	4	4	9
E4390	3874563 (Z81042) similar to Yeast hypothetical protein... +3 228 2.4e	663.817	331.34	2.004	1	3
E5967	548852 40S RIBOSOMAL PROTEIN S21 >pir S38357 ribosom... +1	1143.291	570.93	2.003	2	1
E3310	1707015 (U78721) protein phosphatase 2C isolog [Arabid... +1 425 4	1303.799	650.89	2.003	3	2
E5923	2795.373	1395.32	2.003	2	1	14
E2425	2205.072	1102.8	2	2	4	4
E1814	4586044 (AC007020) putative receptor protein kinase [A... -2 185 1.1	599.156	299.75	1.999	2	12
E896	+3 488 5.3e-	1911.962	956.41	1.999	3	20
E6457	3759184 (AB018441) phi-1 [Nicotiana tabacum]	5586.2	2794.89	1.999	2	1
E5689	3779218 (AF030879) protein kinase CPK1 [Solanum tubero... +3 231	2148.353	1075.93	1.997	2	1
E3133	2941.223	1473.68	1.996	2	1	19
E3809	3892.835	1949.95	1.996	2	1	11
E6249	2451.593	1229.03	1.995	2	1	5
E6731	1156.15	579.96	1.993	2	1	7
E2869	VACUOLAR ATP SYNTHASE	2575.543	1292.89	1.992	1	2
E5417	1576.015	792	1.99	2	1	2
E4006	1947.905	979.12	1.989	2	1	1
E6361	3599415 (AF083190) SPF31 [Homo sapiens]	+1 181 2.9e	855.284	430.27	1.988	4
E6549	4093155 (AF088281) phytochrome-associated protein 1 [A... +1 662	2721.046	1368.53	1.988	1	5
E2761	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN	912.772	459.58	1.986	3	13
E4055	1885.381	949.39	1.986	1	4	1
E934	4678928 (AL049711) putative serine/threonine protein k... +1 791 6.8	792.667	399.29	1.985	3	11
E1902					4	11

E3065	4585976 (AC005287) Unknown protein [Arabidopsis thaliana] +2	298	4173.736	2145.18	1.946	13	21
E4855	G1383		421.681	216.96	1.944	2	2
E5424			807.85	415.93	1.942	1	2
E1156	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+3	586 3.6 ϵ	1471.177	757.51	1.942	4
E694	cystatin B		4546.007	2341.36	1.942	2	10
E4112			373.124	192.19	1.941	4	1
E6671			1085.481	559.37	1.941	1	2
E5186	4678949 (AL049711) dihydrolipoamide S-acetyltransferas...	+2	565 6	4219.827	2174.03	1.941	2
E2555	2132388 PHO85 protein - yeast (Saccharomyces cerevisiae...)	+3	234	5119.299	2637.01	1.941	2
E2949	2245016 (Z97341) hypothetical protein [Arabidopsis tha...	+2	360 3.2	492.865	254.14	1.939	3
E6702	82287 ubiquitin - potato (fragment) >emb CAA77738 (...	+2	77 1.3 ϵ	936.801	483.09	1.939	2
E4764	G10		343.019	177.01	1.938	1	3
E5240	2627238 (D50565) NADH dehydrogenase subunit 5 [Oryza s...	+2	35 ϵ	2149.924	1109.14	1.938	2
E4055	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN			2080.962	1074.52	1.937	2
E5504	3122671 HYPOTHETICAL RAE1-LIKE PROTEIN >pir S71241 pr...	+2	1515.696	783.57	1.934	3	1
E2298			2208.173	1142.14	1.933	1	2
E4692	G727		1325.995	686.62	1.931	3	2
E3378	421941 GTP-binding protein, ras-related - common toba...	+3	226 4.	1501.324	777.38	1.931	1
E600			6670.229	3459.36	1.928	1	2
E4359			448.127	232.54	1.927	3	10
E194			1261.976	654.76	1.927	1	20
E6246	3892056 (AC002330) putative vacuolar ATPase [Arabidops...	+2	625	2481.318	1287.78	1.927	4
E4603	G451		719.286	373.41	1.926	2	20
E4671	G566		450.51	234.07	1.925	2	20
E1949	4539301 (AL049480) putative mitochondrial protein [Ara...	+2	280 6. ϵ	1012.295	525.86	1.925	1
E406	3450842 (AF080436) mitogen activated protein kinase ki...	+1	156 1. ϵ	1555.897	809.27	1.923	2
E384	1351359 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7 ϵ		2371.673	1233.21	1.923	1	8
E4133	A.thaliana cyclophilin		619.789	322.41	1.922	4	14
E5764	1709535 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (2193.699	1141.3	1.922	3	22
E5367	4704730 (AF121355) peroxiredoxin TPx1 [Arabidopsis tha...	+2	190 ;	2900.126	1508.78	1.922	1
E2644	3319353 (AF077407) contains similarity to copper-bindin...	+1	578 2.0 ϵ	893.677	465.45	1.92	2
E5926			2287.164	1192.04	1.919	2	7
E6638	4454472 (AC006234) unknown protein [Arabidopsis thaliana]	+1	605	2905.499	1514.32	1.919	3
E661			1823.28	950.8	1.918	2	6
E1957			4866.036	2537.16	1.918	1	10
E6383	4455246 (AL035523) putative protein [Arabidopsis thali...	+3	676 1.5 ϵ	2764.17	1443.68	1.915	2
E6189	81286 extensin - Volvox carteri (fragment) >emb CAA4...	+1	251 7. ϵ	740.13	386.99	1.913	4

EXHIBIT D

EID	COMMENT	(0.868)CY3CY5	(0.868)CY3METAROWMETACOL
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3 396 4.8e-36 5188.907	445.43	11.649
E986	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23... +2 6776.597	986.01	6.873
E436		4020.197	612.22
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana] +3 330 1.2e-28 20118.45	3072.05	6.549
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2 428 2.0e-	3152.38	5.494
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2 564 7.6e-54 9471.079	1857.32	5.099
E3518	3668173 (AB006777) vegetative storage protein [Arabido... +1 682 1.4e-6 10372.01	2078.74	4.99
E2202		6337.206	1408.07
E1783	45891123 (AF126374) At14a protein [Arabidopsis thaliana] +1 566 4.7e-54 2418.7	559.1	4.326
E6978	3319350 (AF077407) No definition line found [Arabidops... +2 553 1.1e-52 7526.917	1841.41	4.088
E4131	A.thaliana cyclophilin	7765.349	1912.81
E808	2832649 (AL021710) adenylosuccinate lyase - like prote... +2 250 1.4e-28 16343.36	4124.77	3.962
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2 564 7.6e-54 7289.709	1949.31	3.74
E5356	3319350 (AF077407) No definition line found [Arabidops... +3 894 8.1e-89 4843.083	1300.34	3.724
E2228	3413711 (AC004747) putative antifungal protein [Arabid... +3 285 2.8e-24 16292.93	4415.86	3.69
E1759		5466.373	1489.1
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-... +1 528 7.6e-	3016.276	832.96
E3490	2146733 GAST1 protein homolog (clone GASA1) - Arabidop... +2 537 5.5 13064.97	3613.48	3.616
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23... +1 4010.512	1110.75	3.611
E3362	4218987 (AF098630) putative cell wall-plasma membrane ... +3 283 4.6e-	9998.805	2807.89
E6578	2244888 (Z973338) similarity to cytochrome P450 [Arabid... +2 290 4.6e-31 2028.531	570.8	3.554
E3397	4580920 (AF113545) vacuole-associated annexin VCaB42 [... +1 398 5.8e 9304.893	2630.92	3.537
E6937	3319350 (AF077407) No definition line found [Arabidops... +3 539 3.4e-51 7137.625	2026.47	3.522
E3334	3319347 (AF077407) No definition line found [Arabidops... +2 447 3.4e-66 6959.168	2081.01	3.344
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1 293 2.7e-37 5280.938	1640.96	3.218
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara... +2 335 2.1e-3 3011.26	937.67	3.211
E157	2460203 (AF021244) coronatine-induced protein 1 [Arabi... +2 247 3.0e-2 2798.22	916.87	3.052
E4540	G1356	1315.128	431.09
E540	4587542 (AC006577) Belongs to the PF00657 Lipase/Acyl... +3 372 1.7e 7077.355	2394.62	2.956
E2698	629602 probable imbibition protein - wild cabbage >em... +1 256 4.2e-20 14461.7	4898.26	2.952
E2396	1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go... +2 231 5.2e-39 7588.549	2573.92	2.948
E2649	3785997 (AC005499) putative annexin [Arabidopsis thali... +1 595 1.4e-61 3894.893	1340.03	2.907
E2167	4455154 (AL033545) extensin - like protein [Arabidopsi... +2 394 2.7e-50 2498.538	872.22	2.865
E5708	3885331 (AC005623) putative cytochrome p450 protein [A... +2 269 5.6e-	4305.89	2.841

E2546	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3 680 3.9e 8984.748	3163.28	2.84
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1 438 9.7e- 2866.318	1024.66	2.797
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT	11475.71	2.775
E1070	1362093 hypothetical protein (clone TPP15) - tomato (f... +3 471 5.5e-44 4065.957	1487.18	2.734
E5048			
E4767	G7 1181531 (L41244) thionin [Arabidopsis thaliana] >prfl ... +2 430 7.9e-49 3 6683.22	1579.74	2.676
E2678		518.614	199.18
E2153		2619.5	2.604
E4561	3738091 (AC005617) similar to symbiotic ammonium trans... +3 393 1.0e- 1633.45	643.3	2.539
E2477	4510339 (AC006921) putative ABC transporter protein [A... +1 621 8.4e-9 9503.943	3749.84	2.534
E4805		1093.479	432.54
E1523		3351.798	1327.63
E4186	A.thaliana type I chlorophyll a/b binding protein	2943.77	2.546
E3920	4115377 (AC005967) unknown protein [Arabidopsis thaliana] +1 263 1.4e 3075.096	1156.26	2.525
E3115		608.094	243.96
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S666354 ...+2 6 18119.63	1236.49	2.487
E4408		3075.096	1236.49
E350	G350 4734007 (AC007178) hypothetical protein [Arabidopsis t... +3 340 4.0e-40 3976.277	7293.75	2.484
E790		2577.39	2.476
E2444	2578440 (X67425) pectinesterase [Pisum sativum]	892.737	364.7
E4357	+1 147 2.6e-18 12006.51	892.737	364.7
E921		4973.28	2.414
E6269	E6269 2118045 beta-fructofuranosidase (EC 3.2.1.26) - Arabid... +2 929 3.2e-97 3010.973	523.19	2.448
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	1254.43	2.448
E3753	3033.996	1254.43	2.448
E2062156 (AC001645) jasmonate inducible protein isolog ...+2 580 1.6e-55 4825.753	1264.24	2.448	
E6415	2020.85	1264.24	2.448
E4407	5854421 LPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23...+1 3337.514	2415.2	2.448
E6340	G353 576.462	2415.2	2.448
E1918	E6340 2126.46	2415.2	2.448
E1693	E1693 4468807 (AL035601) cytochrome P450 monooxygenase-like ... +3 269 4.2 5711.192	2458.17	2.399
E1654	E1654 1762933 (U66263) tumor-related protein [Nicotiana taba... +3 178 1.5e-25 8887.31	3840.28	2.388
E4710	G1241 9089.632	1409.34	2.368
E2542	E407 3434969 (AB008104) ethylene responsive element binding... +2 422 2.2e- 12955.5	244.81	2.355
E132	E407 4466.357	12955.5	2.346
E2137	E132 3047.595	1912.12	2.336
E2331	3164222 (AB008518) RMA1 [Arabidopsis thaliana] >gi 420... +1 413 7.6e- 11335.91	5626.32	2.303
E1761	E2331 4539330 (AL035679) putative receptor-like protein kina... +1 261 6.5e-21 3547.126	4950.95	2.294
	E1761 602292 (U17987) RCH2 protein [Brassica napus]	1559.21	2.275
	+1 317 4.1e-33 4394.554	1941.1	2.264

E5076	G28	1789.691	790.78
E234	4468813 (AL035601) putative protein [Arabidopsis thaliana]	+3	555 1.5e-58
E3693	26624.348	2926.98	2.263
E3389	399298 STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6...)	+2	3794.505
E2429	4512664 (AC006931) putative ribose phosphate pyrophosphoprotein	+2	193 3.7e-09
E4015	jasmonate inducible protein		2598.641
E3354	2500376 60S RIBOSOMAL PROTEIN L34 >gb AAD14494 (AC005...	+1	4 5697.628
E4014	CATALASE 3		2577.14
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3	396 2.2e-39
E1033	3201632 (AC004669) putative 2A6 protein [Arabidopsis thaliana]	+1	317 4.2e-31
E583	4263704 (AC006223) putative sugar starvation-induced protein	+1	220 2.2e-1
E4015	jasmonate inducible protein		2582.551
E4026	thionin		1756.298
E4026	thionin		816.69
E4015	jasmonate inducible protein		2.151
E175	3192102 (AB013397) polygalacturonase inhibitor [Citrus sinensis]	+2	215 2.7e-27
E3608	3157947 (AC002131) Similar to protein gb Z74962 from B...	+2	564 7.6e-5
E2374	2290532 (U94748) AN11 [Petunia x hybrida]	+1	262 2.2e-28
E5935	2 840 2.8e-100		2
E4585	G1426		4856.161
E4532	G1314		2359.52
E1587	3540183 (AC004122) Highly Similar to branched-chain am...	+1	383 1.9e-09
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana	+3	840 2.8e-100
E2267			4856.161
E4662	G545		1504.016
E2211	32281848 (AL031004) putative protein [Arabidopsis thaliana]	+3	185 1.2e-12
E3047			2620.197
E4835	G1447		1293.62
E1340	39277837 (AC005727) putative core protein [Arabidopsis thaliana]	+3	743 8.3e-73
E1312	3738340 (AC005170) GMP synthase-like protein [Arabidopsis thaliana]	+2	472 4.3e-09
E1477	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GL...		6117.024
E4005	3' flavonoid O-methyltransferase		3579.4
E2628	1946364 (U93215) lipase isolog [Arabidopsis thaliana]	+2	391 6.0e-51
E4349	G921		9675.44
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis thaliana]	+1	125 3.5e-17

E717	3860163 (AF098962) disease resistance protein RPP1-WsA... +2	160	1.4	3477.813	2024.43
E1690	2271485 (AF009647) arginine decarboxylase [Arabidopsis... +3	552	1.4e-2	4356.231	2536.52
E4010	thioredoxin			4332.748	2527.22
E4844	G1006			1176.85	688.53
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana] +2	727	4.0e-71	8355.201	4891.51
E4542	G1363			583.604	342.29
E5665				2090.189	1225.58
E4452	G194			840.139	493.22
E2493				3246.741	1908.09
E6885	3080371 (AL022580) putative pectinacetyl esterase prote... +2	459	9.6e-49	5991.105	3523.77
E4345	G867			2653.929	1562.07
E774	2642159 (AC003000) putative mannose-1-phosphate guanyl... +1	281	1.7	12651.5	7456.91
E4852	G1278			1010.534	595.94
E4045	Myrosinase			3113.983	1837.59
E3683	1170505 EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >... +3	664		2650.805	1565.94
E3769	4218535 (AJ010829) GRAB1 protein [Triticum sp.] +2	493	2.6e-46	3804.224	2251.04
E6788	2911057 (AL021961) caffeoyl-CoA O-methyltransferase - ... +2	516	9.4e-4	1703.639	1008.79
E44	E1928 3127890 (AJ006024) cysteine synthase, O-acetyl-L-serin... +2	182	2.9e-2	4236.586	2516.12
E4503	G859			1403.896	834.07
E5475	3786008 (AC005499) unknown protein [Arabidopsis thaliana] +1	175	4.0e-01	508.165	302.15
E4559	G780			899.488	534.9
E3497	3935167 (AC004557) F17L21.10 [Arabidopsis thaliana] +1	425	4.1e-3	4587.877	2731.62
E3744	282865 chlorophyll a/b-binding protein - Arabidopsis ... +3	600	1.6e-66	2	5548.433
E3777				5483.347	3302.98
E4794	G915			1144.316	3270.13
E5677	3123329 (AJ005929) squalene epoxidase homologue [Arabi... +1	369	9.7e-01	1241.919	548.43
E6301	3915639 ALTERNATIVE OXIDASE 1A PRECURSOR >dbj BAA22625... +1			2274.738	1362.67
E3925	1351272 TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi... +3			2311.039	1386.63
E3641				4923.668	1367.3
E1581	2245055 (Z97342) resistance gene homolog (fragment) [A... +3	519	1.9e-5	1517.207	925.48
E3555				7171.825	912.06
E1088	3402716 (AC004261) unknown protein [Arabidopsis thaliana] +1	204	1.8e-01	5446.4	4311.83
E725	2129648 MYB-related protein 33,3K - Arabidopsis thalia... +3	362	8.6e-62	4013.888	9288.54
E1525	2160152 (AC000375) ESTs gb U75592,gb T43869 ... +2	452	1	925.974	1.663
				559.9	1.654

E1862		2954.498	7420.57	2.512 L28P1A01,L35P119E08
E3403	3913418 S-ADENOSYLMETHIONINE DECARBOXYLASE PRO1	4660.478	11698.55	2.51 L15P8E06,L35P103A02
E3783	2677828 (U93166) cysteine protease [Prunus armeniaca] -1	2601.66	6528.26	2.509 L17P1D10,L35P108F03
E2892		2471.941	6202.71	2.509 L16P2F08,L35P79D12
E1143		511.656	1283.66	2.509 L17P8H01,L35P112D01
E1446	3766368 (AL031907) putative transcription factor, ccr4... +1	157	1376.995	2.508 L20P15H07,L35P115G06
E749	4455274 (AL035527) spliceosome associated protein-like... +1		558.716	2.503 L18P10D08,L35P87D11
E3829	4507433 testis enhanced gene transcript >sp P55061 TEG... +3		8159.658	2.502 L17P1G02,L35P108F09
E3718	3738285 (AC005309) unknown protein [Arabidopsis thaliana] +3		3299.244	2.497 L17P14D03,L35P107A07
E3863	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ... +1		1359.493	2.496 L17P23E05,L35P109D04
E1495	4455208 (AL035440) putative protein [Arabidopsis thali... +1	49.	925.96	2.496 L20P17D01,L35P115H07
E2832	4538928 (AL049483) putative protein [Arabidopsis thali... +1	16	733.718	2.492 L16P1G11,L35P79B06
E2252		628.026	1828.75	2.484 L22P11D02,L35P93F08
E2254	G1181	1112.733	2761.1	2.481 L22P11D07,L35P93F10
E1467	G583	1415.528	3507.02	2.478 L20P10B06,L35P105F02
E3555		1371.352	3395.8	2.476 L16P5F07,L35P105F02
E4663	G525	568.188	1405.36	2.473 J124F07F1
E2171		571.767	1413.42	2.472 L20P7E03,L35P92H11
E1330	1710585 60S ACIDIC RIBOSOMAL PROTEIN P0 >emb CAA637	3130.718	7734.15	2.47 L18P34B06,L35P114D03
E3747	1173221 40S RIBOSOMAL PROTEIN S11-BETA >gi 166869 (L[1375.64	3397.65	2.47 L17P17F05,L35P107H07
E3732	3096939 (AL023094) putative protein [Arabidopsis thali... +2	48	3591.088	2.467 L17P15H06,L35P107C09
E1681	4262173 (AC005508) 3975 [Arabidopsis thaliana]	+3	21 ζ	2.466 L22P24F07,L35P117G07
E1685	2911057 (AL021961) caffeoyl-CoA O-methyltransferase - ... +2		1462.24	2.464 L22P24H04,L35P117G11
E3645	4586248 (AL049640) growth factor like protein [Arabido... +1	3C	797.422	2.462 L16P7H07,L35P106B12
E1282	3063465 (AC003981) F22O13.27 [Arabidopsis thaliana]	+1	1718.745	2.461 L18P27E07,L35P113D08
E1453	1353352 (U31975) alanine aminotransferase [Chlamydomon... +		4230.9	
E713	3063439 (AC003981) F22O13.1 [Arabidopsis thaliana]	+1	961.125	
E3843	3893822 (U96498) ATPase beta subunit [Nicotiana syvest... +1		2365.71	
E3427	2961343 (AL022140) symbiosis-related like protein [Ara... +1	3 ζ	3823.28	2.458 L18P6F11,L35P115A07
E1884	2213592 (AC00348) T7N9.12 [Arabidopsis thaliana]	+3	9397.64	2.454 L18P11E05,L35P87F04
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba... +3	1 ζ	618.504	2.454 L17P21B09,L35P109A01
E1926	2462834 (AF000657) hypothetical protein [Arabidopsis t... +1	17	1517.71	2.452 L16P10A01,L35P103E03
E4379	G532	1609.162	3937.24	2.451 L33P4C06,L35P119H12
E4050	pathogen-inducible protein Cx7c750	843.089	2062.27	2.447 L18P6H02,L35P90G06
E1305		749.827	1833.61	2.446 L18P6F02F1
E1261	4090884 (AF025333) vesicle-associated membrane protein... +3		3378.586	2.445 L18P30A02,L35P113H05
E1949	4539301 (AL049480) putative mitochondrial protein [Ara... +2	2 ζ	3370.44	2.443 L18P4E04,L35P90C11

E1179	1709794	26S PROTEASOME REGULATORY SUBUNIT S5A (M	776.228	1895.97
E472			313.348	765.08
E2764	2244973	(Z97340) similarity to extensin class 1 protei... +2	240	3567.583
E5078	G284		778.975	8703.92
E3733	3128175	(AC004521) unknown protein [Arabidopsis thaliana] +3		1895.26
E720			720.256	1751.75
E1872	4200165	(Y16262) neutral invertase [Daucus carota]	+1	36
E169	114335	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >†		500.034
E2368			1044.219	2532.98
E820	4204313	(AC003027) Icl prt_seq No definition line foun...	+2	49:
E1278			1384.304	3356.34
E4705	G764		49.0.96	1188.29
E3610			1511.947	3658.35
E1882	3540181	(AC004122) Unknown protein [Arabidopsis thaliana] +2		1949.806
E3469			235.698	4714.62
E4747	G666		6321.958	569.01
E1280	1171866	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUB		15256.64
E4736	G839		912.983	2201.59
E2915	4262228	(AC006200) putative receptor protein kinase [A... +3	3	2561.039
E856			1612.518	6173.41
E6526	2529665	(AC002535) putative ribosomal protein L7A [Ara... +2		442.259
E1875	3024697	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1		1883.53
E1265	1703220	ALG2 PROTEIN >gi 127806 (U40857) ALG2 [Arabid...]		4535.94
E901	2369714	(Z97178) elongation factor 2 [Beta vulgaris] +1	453	1446.367
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24_25 PRECURSOR		241.925	3482.65
E3553	4544458	(AC006592) unknown protein [Arabidopsis thaliana] -1		682.059
E3572	2507421	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG		1642.09
E564			2623.425	6310.82
E4380	G526		2411.925	581.47
E1605	G270		1857.054	4461.67
E88			2445.142	5866.67
E1555	2914703	(AC003974) unknown protein [Arabidopsis thaliana] +3		8986.141
E3849	2495365	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >prf 190843		21538.31
E2856			774.849	1855.44
E1661	1362051	protein kinase 3 - soybean >gi 310582 (L19361)... +1		787.08
E3820	2661422	(AJ001342) Putative S-phase-specific ribosomal... +1		1887.569
			2725.053	1884.67
			6522.72	6522.72
			598.778	21538.31
			1432.35	598.778
			557.672	1432.35
			711.195	557.672
			1700.48	711.195
			2481.151	1700.48
			5930.27	2481.151
			1338.972	5930.27
			3199.56	1338.972
			4508.89	3199.56
			935.655	4508.89
			2233.82	935.655
			1510.66	2233.82
			633.42	1510.66
			3670.192	633.42
			8747.75	3670.192

E1235			2861.124	6814.86	2.382 L18P27D06,L35P113D03
E1445			3768.178	8970.52	2.381 L20P15H02,L35P115G05
E1238	2760334 (AC002130) F1N21.5 [Arabidopsis thaliana]	+3 5;	4222.258	10049.8	2.38 L18P27E04,L35P113D06
E3825			425.156	1011.93	2.38 L17P1C05,L35P108E11
E4511	G859		655.695	1560.39	2.38 J123C03F1
E3320	4678226 (AC007135) putative 40S ribosomal protein S14 ... +3		1762.772	4194.1	2.379 L15P5F06,L35P102C01
E6988	4512625 (AC004793) ESTs gb T20423, gb AA712864, gb H76...		419.077	996.78	2.379 J54A12F1
E2042			645.403	1532.97	2.375 L20P11G01,L35P91C08
E3562	3914740 60S RIBOSOMAL PROTEIN L26 >dbj BAA18941 (D78		3452.705	8197.57	2.374 L16P6C05,L35P105H03
E2879			823.363	1954.39	2.374 L16P1H09,L35P79B11
E2143			1363.496	3234.23	2.372 L20P2B03,L35P92D07
E2853	730583 60S ACIDIC RIBOSOMAL PROTEIN P2 >emb CAA550		522.88	1239.76	2.371 L16P5B06,L35P79F03
E5019	G1746		684.744	1623.5	2.371 J128C05F1
E2547	3047119 (AF058919) No definition line found [Arabidopsis... +2 7.		1594.843	3776.45	2.368 L22P8C12,L35P96B01
E1937	2506788 GERANYLGERANYL TRANSFERASE TYPE II BETA, Σ		3346.006	7921.7	2.368 L18P34H06,L35P90A11
E2761	4093155 (AF088281) phytochrome-associated protein 1 [A... +1		944.841	2236.08	2.367 L24P1H05,L35P97F04
E1521	2244909 (Z97339) pyruvate,orthophosphate dikinase [Ara... +1		1897.675	4481.56	2.362 L20P5D12,L35P116D03
E1655			1200.104	2832.85	2.361 L22P14C07,L35P117B11
E763			858.316	2023.86	2.358 L18P15H01,L35P87G07
E2341	2618701 (AC002510) hypothetical protein [Arabidopsis t... +2 4;		1144.044	2694.13	2.355 L22P1F01,L35P94E09
E4679	G632		434.714	1020.65	2.348 J124H07F1
E4839	4544394 (AC007047) hypothetical protein [Arabidopsis t... +3 6:		964.742	2264.46	2.347 J126D07F1
E3159	4262232 (AC006200) putative ribosomal protein L7 [Arab... +2		2259.313	5300.94	2.346 L15P3G08,L35P101C03
E1992			2374.241	5569.31	2.346 L20P10C03,L35P91B06
E3239			2018.283	4729.6	2.343 L15P5A10,L35P101H11
E4458	G179		106.003	248.34	2.343 J122D12F1
E5108	G760		736.055	1722.49	2.34 J129F02F1
E3012	927577 (U12927) alpha-galactosidase [Phaseolus vulgaris] +3		3468.416	8104.18	2.337 L33P3C07,L35P98H12
E3464	1168319 ACTIN 1 >gi 169909 (J01298) actin [Glycine max] +2		6255.594	14606.09	2.335 L15P9D01,L35P103C10
E2280			1771.759	4132.58	2.332 L22P16F01,L35P94B06
E279	2460318 (AF021819) RNA-binding protein regulatory subu... +1		3038.91	7087.01	2.332 L17P1D04,L35P82F07
E3234	1076580 alcohol dehydrogenase homolog ADH3b - tomato > ... +		478.878	1116.73	2.332 L15P4H07,L35P101G12
E4966	G1523		156.419	364.6	2.331 J127G08F1
E3372	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +2 5		5696.717	13277.42	2.331 L15P5H06,L35P102C11
E4852	G1278		536.155	1249.5	2.33 J126F09F1
E3215	3080427 (AL022604) putative protein [Arabidopsis thali... +3 56		2247.89	5228.07	2.326 L15P4C03,L35P101D11
E2627			1208.37	2808.93	2.325 L23P1G09,L35P96H08

E3526	4128208 (AF076277) ethylene response factor 1 [Arabido... +1	4528.856	10477.79
E2385	4128208 (AF076277) ethylene response factor 1 [Arabido... +1	871.231	2015.07
E4009	major latex protein	413.732	956.39
E3586	1350720 60S RIBOSOMAL PROTEIN L32	+1	2867.786
E1738		5(6621.35
E1228	3892056 (AC002330) putative vacuolar ATPase [Arabidops... +2		845.526
E4746	G1300		1952.08
E3579	1705677 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >pir		669.591
E2037	3395425 (AC004683) putative DNA binding protein [Arabi... +1		1545.09
E3084			829.739
E2452	2500347 NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >		1913.51
E3170	464707 40S RIBOSOMAL PROTEIN S18 >pir S37496 ribosom.		5504.922
E5369	2661422 (AJ001342) Putative S-phase-specific ribosomal... +2		12689.05
E1270	4008441 (AL034488) predicted using Genefinder, cDNA ES... +2		2948.097
E3687	2262104 (AC002343) unknown protein [Arabidopsis thaliana] +1		2495.197
E1687			2948.097
E152			829.739
E758	549577 HYPOTHETICAL 17.1 KD PROTEIN IN MECB-GLTX IN		1913.51
E3249	2764941 (X98255) transcriptionally stimulated by gibbe... +1		5504.922
E5450	3451073 (AL031326) putative protein [Arabidopsis thali... +3		12689.05
E3260	2129629 L-ascorbate peroxidase (EC 1.11.1.11) - Arabid... +1		2948.097
E4676	G649		2495.197
E3205			2948.097
E1427	G467		829.739
E2489			1913.51
E3852	3746809 (AF082882) adenylyl kinase [Arabidopsis thali... +1		5504.922
E4567	G1033		12689.05
E3743	3929649 (AJ131205) mitochondrial NAD-dependent malate ... +2		2948.097
E4381	G528		12689.05
E3715	133872 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PREI		2495.197
E1668	2146740 inner mitochondrial membrane protein - Arabido... +2		12689.05
E4366	G157		2948.097
E5130	Bad Sequence, Maybe G173		12689.05
E1451	2911039 (AL021961) cinnamyl alcohol dehydrogenase - II... +3		1517.069
E1571	4455186 (AL035521) putative protein [Arabidopsis thali... +3		1517.069
E5007	3790587 (AF079182) RING-H2 finger protein RHF2a [Arabi... +1		180.832
E4900	G370		408.65

E5441	133872	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PREI		477.946	1079.68	2.259 J18G10F1
E1488	4371281	(AC006260) hypothetical protein [Arabidopsis thaliana]; +1		725.899	1639.44	2.258 L20P15B04,L35P115F12
E3185	3193285	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]; +1		3504.252	7913.63	2.258 L15P4G06,L35P101G05
E946	2129944	RNA-binding protein RZ-1 - wood tobacco >dbj B...+1		4098.828	9254.98	2.258 L18P32B02,L35P89E10
E1691	4455287	(AL035527) putative protein [Arabidopsis thaliana]; +1	23	2027.805	4574.28	2.256 L22P2D11,L35P117H11
E3831	3643604	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]; -2	20	2797.917	6309.99	2.255 L17P1G05,L35P108F11
E1266				928.446	2093.44	2.255 L18P1H04,L35P113A10
E1612	1709498	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pir E1169		1153.591	2598.37	2.252 L22P16H05,L35P117C04
E1169	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]; +2	€	1423.98	3202.82	2.249 L18P17A06,L35P112H03
E2351				1308.133	2939.28	2.247 L22P21F03,L35P94G07
E2369				1090.309	2443.58	2.241 L22P2A06,L35P95C04
E2865	3184292	(AC004136) putative nucleic acid binding protein [Arabidopsis thaliana]; +1	2	1247.188	2794.69	2.241 L16P5F12,L35P79H03
E2070				1550.17	3471.67	2.24 L20P15F08,L35P91G12
E5048				351.508	786.79	2.238 J128F11F1
E4660	G464			250.054	559.3	2.237 J124F09F1
E3211				2154.839	4819.73	2.237 L15P4B05,L35P101D07
E2273				1073.417	2399.72	2.236 L22P14D05,L35P94A05
E1189				1151.067	2573.31	2.236 L17P9E04,L35P112D11
E5417				485.342	1084.55	2.235 J18A10F1
E677	4512673	(AC006931) putative phosphoprotein phosphatase...+1		670.909	1498.8	2.234 L17P7F09,L35P86H10
E3621	585777	GTP-BINDING NUCLEAR PROTEIN RAN1 >gi 453561		5504.835	12294.42	2.233 L17P11C02,L35P106F06
E5325	3859607	(AF104919) contains similarity to cysteine protease...+3	32	823.176	1838.08	2.233 J56E11F1
E1878	2342734	(AC002341) DNA-binding protein isolog [Arabidopsis thaliana]; +3		953.443	2127.86	2.232 L28P3G04,L35P119G12
E5043				390.836	871.85	2.231 J128F05F1
E198	2501102	SYNTAXIN-RELATED PROTEIN KNOLLE >gi 118416€		1919.527	4281.47	2.23 L17P17A12,L35P81H09
E3749	4337178	(AC006416) T31J12.5 [Arabidopsis thaliana]; +3	4	1439.12	3203.42	2.226 L17P17F12,L35P107H09
E5111				171.845	382.48	2.226 J129F11F1
E4308	G306			209.918	466.76	2.224 J121B01F1
E2052	G1111			1055.779	2344.96	2.221 L20P13A06,L35P91D12
E392	643469	(U19886) unknown [Lycopersicon esculentum]; +1		1979.601	4396.32	2.221 L17P25H04,L35P83H12
E4828	G1379			834.202	1851.49	2.219 J126C09F1
E5781				2964.952	6577.41	2.218 J28F11F1
E3231	1173218	40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461		1744.214	3869.13	2.218 L15P4H03,L35P101G09
E1236	2244827	(Z97336) hypothetical protein [Arabidopsis thaliana]; +2	41	3339.604	7406.49	2.218 L18P27D11,L35P113D04
E4939	G1232			200.508	444.62	2.217 J127A05F1
E669	1304227	(D63781) Epoxide hydrolase [Glycine max]; +1		1038.029	2301.67	2.217 L17P7B04,L35P86G08
E3830	1550738	(Y08061) endomembrane-associated protein [Arabidopsis thaliana]; +		3476.881	7706.32	2.216 L17P1G04,L35P108F10

E1774	3122572	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUB	1906.43	4217.14	2.212 L23P1C04,L35P118F10
E4357	G921		491.209	1086.46	2.212 J121H09F1
E1611	2623297	(AC002409) unknown protein [Arabidopsis thaliana... +1	3975.548	8789.49	2.211 L22P16B02,L35P117C03
E1347	2262098	(AC002343) HSP90 isolog [Arabidopsis thaliana] +3	1163.97	2571.05	2.209 L18P4H08,L35P114G02
E3864	4160402	(AJ132240) eukaryotic translation initiation f... +1	236	555.695	2.207 L17P23F02,L35P109D05
E1762			665.552	1468.51	2.206 L22P9D12,L35P118D10
E3908	1172977	60S RIBOSOMAL PROTEIN L18 >gil606970 (U15741)	318.258	701.88	2.205 L17P23H08,L35P109D07
E2425			1201.148	2648.19	2.205 L22P4D01,L35P95E11
E3291	728880	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARI	1110.309	2447.82	2.205 L34P2D10,L35P120C09
E1275	3269293	(AL030978) putative protein [Arabidopsis thali... +1	51.	1736.396	2.202 L18P26A04,L35P113C07
E3463	3123188	CATALASE 3 >gil2347178 (U43147) catalase 3 [Ar... +:	13022.707	28658.02	2.201 L15P9C05,L35P103C09
E3190	4689473	(AC007213) putative receptor protein kinase [A... +2	4	1704.103	3748.35
E1185	2674203	(AF036328) CLP protease regulatory subunit CLP... +1	1239.37	2726	2.2 L15P5A01,L35P101H04
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR		482.943	1060.41	2.2 L17P9B11,L35P112D07
E3271			1099.669	2413.11	2.196 L20P2D01F1
E3860	3785983	(AC005560) hypothetical protein [Arabidopsis t... +3	9	1068.669	2.194 L34P8G01,L35P120F01
E4925	G394		169.868	372.44	2.193 L17P23C11,L35P109D01
E2782		cyclophilin	1330.643	2917.1	2.193 J127G02F1
E4040			1409.102	3088.32	2.192 L23P2G07,L35P97B07
E2766			1679.404	3680.5	2.192 L24P1C03,L35P97G03
E2757			677.087	1483.14	2.19 L23P9F05,L35P97E06
E1565	2347191	(AC002338) DNA binding protein isolog [Arabido... +3	1685.582	3690.55	2.189 L20P4B05,L35P116C11
E1866	4538920	(AL049483) nitrogen fixation like protein [Ara... +2	164	2317.834	2.189 L28P1B07,L35P119E12
E3157			1142.056	2499.1	2.188 L15P3G05,L35P101C01
E3916	4582460	(AC007071) unknown protein [Arabidopsis thaliana] +3	905.488	1979.88	2.187 L17P25C02,L35P109E09
E4894	G743		2418.927	5284.23	2.185 J127C10F1
E3210	1546688	(X98802) peroxidase ATP11a [Arabidopsis thalia... +2	962.38	2101.1	2.183 L15P4A02,L35P101C12
E2909			948.732	2071.1	2.183 L16P5F04,L35P79G11
E5968	285286	flavonol 4'-sulfotransferase - Flaveria chlora... +2	218	844.519	2.181 J34C08F1
E566	2213626	(AC00103) F21J9.18 [Arabidopsis thaliana]	+2	1651.946	2.181 L17P37G07,L35P85F07
E3415	4056502	(AC005896) 40S ribosomal protein S5 [Arabidops... +1	6229.491		2.18 L15P9A10,L35P103C03
E6508	2088653	(AF002109) Hs1pro-1 related protein isolog [Ar... +3	5	784.532	2.18 J44B12F1
E3868	4454026	(AL035394) phosphatase like protein [Arabidops... +1	2000.285	4357.83	2.179 L17P25B04,L35P109E03
E1468	4510375	(AC007017) putative homeotic protein BEL1 [Ara... -1	1407.647	3066.69	2.179 L20P10H03,L35P115C10
E3229	1524370	(X92491) TOM20 [Solanum tuberosum]	+2	651.419	2.177 L15P4H01,L35P101G07
E4505	G773		244.026	530.99	2.176 J123B04F1
E1643			634.452	1379.26	2.174 L22P26F02,L35P117H05

E4057	glutamate--ammonia ligase	2.174	L20P2E04F1	
E4765	G620	2.173	J125E07F1	
E2202		2.173	L22P10A07,L35P93E06	
E1114	G1745	2.173	L17P41D01,L35P111C10	
E1432	4185513 (AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] +3	5	2.172	L20P13G06,L35P115E04
E2408	E1338 (D49738) cytoskeleton associated protein [Homo sapiens] +1		2.171	L22P28B04,L35P95B12
E3368	464621 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >pir S28..		2.171	L15P5G08,L35F102C07
E4510			2.167	J123C10F1
E3090	3785989 (AC005560) unknown protein [Arabidopsis thaliana] +3		2.166	L34P2F05,L35P99G06
E538			2.166	L17P30F08,L35P85A09
E2491			2.166	L15P7D11,L35P77H05
E4053	endochitinase	2.165	L18P8B07F1	
E143	4105698 (AF049870) small hydrophobic protein [Arabidopsis thaliana] +2		2.164	L17P16C06,L35P81G02
E302	2529229 (AB007907) 6-phosphogluconate dehydrogenase [Glycine max] +1		2.164	L17P20F09,L35P83A06
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Araidopsis thaliana] +3		2.164	L15P9H03,L35P103D11
E3111	4567281 (AC006841) unknown protein [Arabidopsis thaliana] +3		2.162	L33P7F04,L35P99C09
E1283	3252815 (AC004705) vacuolar sorting receptor-like protein... +3	51	2.162	L18P27E10,L35P113D09
E1855	3695383 (AF096370) similar to inorganic pyrophosphatases... +3		2.16	L24P6H06,L35P119D07
E3581	2511576 (Y13177) multicatalytic endopeptidase [Arabidopsis thaliana] +1	7	2.16	L16P6E09,L35P105H07
E2406			2.159	L22P28A08,L35P95B10
E3329	730645 40S RIBOSOMAL PROTEIN S15 >pir S43412 ribosom.		2.158	L15P6B09,L35P102D04
E1593			2.158	L15P10A10,L35P116H09
E3667	2529665 (AC002535) putative ribosomal protein L7A [Arabidopsis thaliana] +2		2.158	L22P10A10,L35P120D07
E4502	G804	2.158	L34P4F04,L35P121D03	
E4710	G1241	2.156	L17P9A01,L35P112D03	
E1145		2.155	J123B10F1	
E2606		2.155	J125D10F1	
E2748		2.155	J22P9D09,L35P96D07	
E969	2702268 (AC003033) putative cellulase [Arabidopsis thaliana] +3	3	2.153	L23P6B07,L35P97D03
E5147	E4498 G702	2.152	L17P28B01,L35P110A03	
E3041		2.151	J129E07F1	
E2538	2129899 chalcone reductase homolog - Sesbania rostrata... +1		2.151	L34P8G07,L35P100B11
E1796	E2398 2104683 (X97908) transcription factor [Vicia faba]	+1	2.15	L15P7G02,L35P77H10
E2391	2252854 (AF013294) similar to auxin-induced protein [Arabidopsis thaliana] +1	1	2.149	L24P10B02,L35P119B02
			2.149	L22P6C05,L35P95G02

E6020	1723239 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHF	419.587	901.27	2.148 J34H12F1
E3483	4455235 (AL035523) PROTEIN TRANSPORT PROTEIN SEC61	4100.494	8804.03	2.147 L16P10G01,L35P103F11
E5076	G28	1573.961	3378.84	2.147 J129B02F1
E2429	4512664 (AC006931) putative ribose phosphate pyrophosp... +2	397.201	852.09	2.145 L22P5H09,L35P95F09
E521		1257.108	2695.84	2.144 L17P37D02,L35P85F03
E4960	G1713	227.084	486.93	2.144 J127F06F1
E1985		945.276	2026.53	2.144 L18P8F06,L35P91A05
E1500	2088653 (AF002109) Hs1pro-1 related protein isolog [Ar... +3	5	2620.554	2.144 L20P1A07,L35P115H12
E1724		5617.62	300.831	2.14 L23P12F07,L35P118F02
E1101	127045 S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIC	1501.332	3212.64	2.14 L17P3A07,L35P111A08
E1579	118619 SUCCINATE DEHYDROGENASE (UBIQUINONE) IRO1	1317.182	2817.86	2.139 L21P1F04,L35P116F07
E4683	G660	1438.486	3074.89	2.138 J125A01F1
E2743	3152621 (AC004482) cold acclimation protein WCOR413-li... +2	1768.44	3780.12	2.138 L23P3D08,L35P97C04
E1832		5688.065	12148.83	2.136 L28P4E07,L35P119H02
E4856	G378	435.945	931.03	2.136 J126F11F1
E1543	1170028 GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE	2243.192	4790.25	2.135 L21P8B05,L35P116H01
E1303		2560.082	5457.98	2.132 L18P2G12,L35P113G11
E1650		492.874	1050.73	2.132 L22P12C01,L35P117A12
E1562	3164138 (D78604) cytochrome p450 monooxygenase [Arabid...]	1158.215	2469.11	2.132 L20P2G05,L35P116C08
E3124		2277.822	4855.72	2.132 L34P1E08,L35P99E10
E2297	1778095 (U64903) putative sugar transporter; member of ... +3 :	4428.944	9439.68	2.131 L22P1E02,L35P94E05
E1449	1046225 (U21952) ethylene response sensor [Arabidopsis... +3	1768.888	3769.85	2.131 L20P17B08,L35P115H03
E1935	4210330 (AJ223802) 2-oxoglutarate dehydrogenase, E1 su... +2	3572.654	7611.53	2.13 L18P34G06,L35P90A09
E5422	1168748 CALMODULIN-4 >pir S35185 calmodulin 4 - Arabi... +2	1110.048	2363.31	2.129 J18B11F1
E551		1805.457	3843.1	2.129 L17P32G10,L35P85C10
E2682	3702964 (AF079485) rac GTP binding protein Arac10 [Ara... +1	2377.647	5057.39	2.127 L15P8B04,L35P78A09
E5015		309.32	657.58	2.126 J128B07F1
E548		2167.083	4602.66	2.124 L17P32E09,L35P85C07
E2377		822.182	1746.03	2.124 L22P2G04,L35P95D06
E2512		1607.708	3413.64	2.123 L15P4H09,L35P77D08
E1486		1765.209	3747.91	2.123 L20P14H07,L35P115F10
E3144	4454472 (AC006234) unknown protein [Arabidopsis thaliana] +1	2387.529	5068.22	2.123 L34P4G03,L35P99H12
E6947	730645 40S RIBOSOMAL PROTEIN S15 >pir S43412 ribosom.	776.291	1647.64	2.122 J51H04F1
E3261	2894599 (AL021889) putative protein [Arabidopsis thali... +1	58	4151.73	2.122 L34P3G03,L35P120D03
E1209	1495269 (X97829) product similar to ccr protein, Citru... +1	387	2150.476	2.118 L18P17E02,L35P112H07
E3462	G860	1541.755	3265.62	2.118 L15P9C02,L35P103C08
E1464	G512	984.729	2085.73	2.118 L18P9B08,L35P115B12

E4774	G301		707.32	2.116 J125G08F1
E4766	G563	419.463	887.65	2.116 J125E08F1
E759		2697.595	5708.38	2.116 L18P15C02,L35P87F09
E521		657.771	1391.33	2.115 L17P37D02,L35P85F03
E3739	3450889 (AF083890) 19S proteasome subunit 9 [Arabidopsis... +3	1482.165	3134.05	2.115 L17P17A03,L35P107F09
E4336	G519	1541.27	3253.09	2.111 J121E03F1
E2210	2943789 (AB000875) RD22BP1 [Arabidopsis thaliana] +1 ;	1947.855	4110.53	2.11 L22P11G06,L35P93G02
E2781	1170203 GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GL	1513.352	3192.79	2.11 L23P2D09,L35P97A12
E1269	3335333 (AC004512) Similar to chloroplast membrane-ass... +2	2124.783	4472.16	2.105 L18P23D02,L35P113B07
E4017	UBIQUITIN-CONJUGATING ENZYME	466.796	982.07	2.104 L15P9G10F1
E1834	4406780 (AC006532) putative multispanning membrane pro... +2	1854.158	3899.35	2.103 L33P3B02,L35P119H04
E1409	133709 CYANELLE 30S RIBOSOMAL PROTEIN S10 >pir R3K	2422.817	5089.72	2.101 L18P6E05,L35P115A05
E4025	CELL DIVISION CYCLE PROTEIN 48	927.738	1945.98	2.098 L16P11D01F1
E1644		1399.22	2934.35	2.097 L22P28B06,L35P117H06
E3508	4193382 (AF083336) ribosomal protein S27 [Arabidopsis ... +3	2651.231	5558.39	2.097 L16P1G05,L35P104D06
E1489		1333.092	2794.08	2.096 L20P16B07,L35P115G07
E5101	cafeic o-methyltransferase	302.459	633.89	2.096 J129E10F1
E4069	G1398 (similar to remorin 1)	805.165	1687.13	2.095 L34P4G06F1
E1873		1100.838	2304.93	2.094 L28P2H04,L35P119G07
E3721	2829891 (AC002311) Unknown protein [Arabidopsis thaliana] +2	409.842	858.09	2.094 L17P14D11,L35P107A10
E6744		497.883	1041.47	2.092 J46C06F1
E2292		2303.117	4817.58	2.092 L22P1A07,L35P94D06
E757		1150.334	2405.79	2.091 L18P15A05,L35P87F07
E4526	G1125	1400.686	2928.99	2.091 J123E10F1
E3725	3892714 (AL033545) trehalose-6-phosphate phosphatase -... +1	2128.786	4450.72	2.091 L17P15C09,L35P107B08
E2896	2739383 (AC002505) unknown protein [Arabidopsis thaliana] +1	1579.306	3299.84	2.089 L16P5A03,L35P79E10
E1229		240.148	501.65	2.089 L18P25C09,L35P113C03
E3550		5788.835	12070.32	2.085 L16P5B01,L35P105C04
E3208	4586109 (AL049638) putative protein [Arabidopsis thali... +3 27:	5072.706	10576.02	2.085 L15P3H08,L35P101C10
E2436	2578442 (X67426) pectinesterase [Pisum sativum] +2 11	1518.162	3164.27	2.084 L22P6E11,L35P95G10
E1447	2832241 (AF030864) nonphototropic hypocotyl 1 [Arabido... +2	4618.825	9624.53	2.084 L20P16H05,L35P115H01
E1471		2029.234	4227.41	2.083 L20P11G04,L35P115D07
E985	1174870 UBIQUINOL-CYTOCHROME C REDUCTASE COMPL	1615.949	3365.97	2.083 L17P2H04,L35P110D01
E855	3608412 (AF079355) protein phosphatase-2c [Mesembryant... +;	2227.555	4639.52	2.083 L18P27G03,L35P88F09
E2752	1362162 beta-glucosidase BGQ60 precursor - barley >gil... +3 ;	4572.784	9520.91	2.082 L23P9B01,L35P97E01
E1735	2351374 (U54560) putative 26S proteasome subunit athMO... +1	1149.514	2392.79	2.082 L23P2G02,L35P118H01
E3738	4127456 (AJ010818) Cpn21 protein [Arabidopsis thaliana] +2 ;	4289.48	8927.44	2.081 L17P16F09,L35P107E09

E6201	2511598 (Y13696) multicatalytic endopeptidase complex,... +2 :	680.02	1414.87	2.081 J37F05F1
E4712	G10233	221.217	460.13	2.08 J125D11F1
E338	3915847 40S RIBOSOMAL PROTEIN S2 >j 2335095 (AC00235:	632.538	1314.6	2.078 L17P25A05,L35P83G06
E5135		1072.51	2228.46	2.078 J129B07F1
E1647		911.579	1893.87	2.078 L22P11G05,L35P117A09
E2343	541849 anthranilate synthase (EC 4.1.3.27) beta chain... +3 36	2272.017	4720.09	2.077 L22P1F05,L35P94E11
E4854	G1366	591.307	1228.15	2.077 J126F10F1
E4503	G859	583.899	1212.3	2.076 J123B03F1
E4680	G656	375.485	779.37	2.076 J124H11F1
E1073		947.104	1964.64	2.074 L17P40B02,L35P111C02
E4492	G1390	322.608	668.69	2.073 J123A09F1
E2618		1265.088	2620.9	2.072 L23P12E08,L35P96F08
E4007	CYSTEINE PROTEINASE 2 PRECURSOR	458.17	949.15	2.072 L15P6D02F1
E191	2459438 (AC002332) hypothetical protein [Arabidopsis t... +1 2(1640.623	3395.79	2.07 L17P16E03,L35P81G08
E1778		730.635	1511.54	2.069 L23P2D03,L35P118G08
E3008	2341039 (AC000104) Similar to Nicotiana lesion-inducin... +1 4:	4083.452	8446.91	2.069 L33P3B01,L35P98H08
E1391	2739389 (AC002505) Cf-2.2 like protein [Arabidopsis th... +1 57	2451.344	5065.38	2.066 L18P4G06,L35P114F11
E690		1187.288	2453.06	2.066 L17P9B10,L35P87B05
E4050	pathogen-inducible protein CxC750	2748.309	5677.92	2.066 L18P6F02F1
E4468	G1352	433.956	896.08	2.065 J122F09F1
E2403	2642432 (AC002391) putative elicitor response element ... +2 2	1748.751	3610.71	2.065 L22P26E08,L35P95B07
E1798	4335735 (AC006248) hypothetical protein [Arabidopsis t... +2 3:	796.576	1643.14	2.063 L24P12A01,L35P119B04
E3082	4567260 (AC006841) putative NADPH dependent mannose 6...	2439.411	5030.77	2.062 L34P1G10,L35P99F04
E1792	3717946 (AJ005901) vag1 [Arabidopsis thaliana]	+2 404	3429.697	2.061 L23P7B01,L35P119A04
E2456		3200.078	6595.41	2.061 L15P3G11,L35P77B06
E4071	cruciferin 1	632.239	1302.29	2.06 L34P9H04F1
E2014	3128195 (AC004521) putative phosphoribosyl pyrophospho... +1	1524.626	3138.81	2.059 L20P14D03,L35P91F04
E1149	4006829 (AC005970) putative protein kinase [Arabidopsi... +3 4	977.557	2011.9	2.058 L17P9G03,L35P112E01
E2054		3046.865	6270.71	2.058 L20P14A07,L35P91E08
E4556	G658	303.329	624.13	2.058 J123A06F1
E2065	3810848 (AL032684) putative autophagy protein [Schizosaccharomyces pombe] +1 27:	2845.624	5851.22	2.056 L20P15C08,L35P91G07
E2727	4678226 (AC007135) putative 40S ribosomal protein S14 ... +2	1158.463	2381.64	2.056 L16P1B03,L35P78H12
E2212		1417.479	2913.56	2.055 L22P12C03,L35P93G04
E2214	4455293 (AL035528) putative protein [Arabidopsis thaliana]	1134.399	2331.57	2.055 L22P12E05,L35P93G06
E3384	1351359 UBIQUINOL-CYTOCHROME C REDUCTASE COMPL	1798.558	3696.64	2.055 L15P7C04,L35P102E11
E3319	3024434 26S PROTEASE REGULATORY SUBUNIT 6A HOMO1	986.072	2026.31	2.055 L15P5E02,L35P102B06
E3895	4467128 (AL035538) putative protein [Arabidopsis thaliana]	+3 47:	716.875	1472.32

E1861	3287693 (AC003979) Similar to LM17 gene product gb 16...+2	2338.666	4801.31	2.053 L24P9E08,L35P119E07
E2601	135535 T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-Al	2325.776	4774.42	2.053 L22P8H07,L35P96C08
E4519	G1009	215.946	442.81	2.051 J123D03F1
E1187	1841355 (D85381) cytochrome c oxidase subunit Vb precu...+1	940.13	1927.06	2.05 L17P9D02,L35P112D09
E1157	2809245 (AC002560) F21B7.14 [Arabidopsis thaliana]	+2 8	1393.117	2.049 L18P10E06,L35P112F03
E2098	3702336 (AC005397) putative 3-methyl-2-oxobutanoate hy...+1	871.33	1785.16	2.049 L20P1H05,L35P92D04
E2450	4646206 (AC007230) Contains similarity to gb D13630 Kl...+3	1856.084	3802.35	2.049 L15P3B02,L35P77A06
E2829	4567201 (AC007168) putative aspartate aminotransferase...+1	5126.379	10497.97	2.048 L16P1G01,L35P79B03
E5411	4455223 (AL035440) putative DNA binding protein [Arabi...+3	785.352	1607.49	2.047 J18G08F1
E3919	3128228 (AC004077) putative ribosomal protein L18A [Ar...+1	1340.563	2742.47	2.046 L17P25C10,L35P109E12
E669	1304227 (D63781) Epoxide hydrolase [Glycine max] >emb ...+1	1660.871	3396.49	2.045 L17P7B04,L35P86G08
E4109	GP-39	5938.53	12138.75	2.044 O17203,M80927
E3378	421941 GTP-binding protein, ras-related - common toba...+3	4026.051	8229.36	2.044 L15P6D11,L35P102D11
E3110		1075.07	2196.51	2.043 L33P7E03,L35P99C08
E3293		437.014	892.06	2.041 L34P2E04,L35P120C11
E2431		2207.157	4502.44	2.04 L22P6A09,L35P95F11
E1126		1157.941	2361.03	2.039 L17P5H03,L35P111E10
E1824		1093.131	2226.94	2.037 L28P1F03,L35P119F06
E2200		654.191	1331.93	2.036 L22P10A04,L35P93E04
E333		1206.828	2456.71	2.036 L17P23H04,L35P83G01
E1816	4103987 (AF030516) 5,10-methylenetetrahydrofolate dehy...+1	5051.749	10282.53	2.035 L24P9A06,L35P119E04
E2564		1186.928	2414.88	2.035 L22P9D08,L35P96D06
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t...+1	1	2534.973	2.035 L15P5G07,L35P77F04
E1796		1494.719	3039.63	2.034 L24P10B02,L35P119B02
E2146	1170409 HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HC	1511.226	3071.03	2.032 L20P2C01,L35P92D10
E3151	2499811 PROFILIN 2 >gi 1353766 (U43323) profilin 2 [Ar...+1	5361.032	10890.84	2.031 L15P3C10,L35P101B01
E517	4204311 (AC003027) lclprt_seq No definition line foun...+2	64!	650.574	2.03 L17P36F06,L35P85E05
E644	4753657 (AL049751) putative protein [Arabidopsis thali...+3	33	576.814	2.028 L17P41D03,L35P86C07
E1885	1084415 RNA-binding protein - Wood tobacco >db BAA051...+2	3681.367	7465.9	2.028 L18P34F02,L35P90A01
E0	NUL	186.363	377.79	2.027 NUL
E533		1675.265	3394.21	2.026 L17P3B11,L35P85H04
E2976	1173351 DNA BINDING PROTEIN S1FA >pir S47063 s1Fa pro.	2964.591	5989.77	2.02 L24P9F06,L35P98B12
E4309		225.057	454.62	2.02 J121B09F1
E2207	3688173 (AL031804) putative protein [Arabidopsis thali...+2	47	928.086	2.019 L22P11B08,L35P93F05
E1461		1155.853	2333.24	2.019 L18P9A02,L35P115B09
E2689	4678261 (AL049657) putative proteasome regulatory subu...+2	2133.509	4303.84	2.017 L15P8E08,L35P78B10
E579		597.038	1203.67	2.016 L17P3C09,L35P85H08

Coord	EID	ANNOTATION cy3_cut 6378_88 cy5_cut 6073.95	N.Cy3	Cy5	N.Cy3/Cy5 Cy5/N.Cy3 Ig2(N.3/5)
4_1_22_1 E0			886.84	28.22	31.42 0.03 4.97
1_1_9_17 E5137	2129662 ovule-specific homeotic protein homolog A20 - ... +3	141 8	957.03	45.26	21.15 0.05 4.4
1_1_17_6 E3171	481821 probable glutathione transferase (EC 2.5.1.18)...+3	586 3.€	37174.02	1936.59	19.2 0.05 4.26
4_4_11_5 E53			684.54	39.7	17.24 0.06 4.11
3_1_22_18 E7257	G671	541849 anthranilate synthase (EC 4.1.3.27) beta chain...+3	367 1.€	2754.52	312.13 8.82 0.11 3.14
1_2_15_8 E2343	G1537		7420.95	913.06	8.13 0.12 3.02
3_1_21_23 E7183			2484.58	378.37	6.57 0.15 2.72
2_4_15_13 E2623	4467097 (AL035538) heat shock protein 70 like protein ...+3	584 5.!	3715.08	603.15	6.16 0.16 2.62
3_1_1_15 E4060	"chlorate/nitrate transporter,"		1431.23	234.47	6.1 0.16 2.61
2_3_19_22 E1454	3688186 (AL031804) putative protein [Arabidopsis thali...+3	676 1.1	8146.8	1338.85	6.08 0.16 2.61
4_1_7_11 E4349	G921		1620.41	270	6 0.17 2.59
2_2_20_8 E1525	2160152 (AC000375) ESTs gb U75592.gb T43869 ...+2		7303.89	1299.66	5.62 0.18 2.49
4_2_7_11 E4357	G921		2627.14	471.47	5.57 0.18 2.48
3_4_8_15 E4794	G915		11557.62	214.3	5.39 0.19 2.43
3_3_22_4 E7204	G1420		499.89	93.83	5.33 0.19 2.41
2_3_7_21 E4564	G920		777.56	152.68	5.09 0.2 2.35
4_1_13_23 E2049	3851530 (AF065435) nodulin [Glycine max]	+3 640 6.8e-{	7283.43	1541.02	4.73 0.21 2.24
1_1_10_4 E5114	G915		17693.16	3799.43	4.66 0.21 2.22
1_2_8_16 E4827	G186		7865.42	1726.66	4.56 0.22 2.19
1_3_11_18 E123	38822356 (U92460) 12-oxophytodienoate reductase OPR2 [A...+3	53	4076.81	897.31	4.54 0.22 2.18
1_2_19_20 E1312	3738340 (AC005170) GMP synthase-like protein [Arabidop...+2 472		16921.24	3731.98	4.53 0.22 2.18
1_4_16_18 E3313	464367 POLYGALACTURONASE INHIBITOR PRECURSOR (POLYI		9413.85	2106.11	4.47 0.22 2.16
1_1_9_13 E5067			7702.47	1753.09	4.39 0.23 2.14
1_2_21_21 E7448			8179.46	1861.13	4.39 0.23 2.14
3_1_20_23 E1669	3834312 (AC005679) Strong similarity to glycoprotein E...+1	595 1.!	25818.04	5998.3	4.3 0.23 2.11
4_4_12_13 E784	3420008 (AF000307) steroid sulfotransferase 3 [Brassic...+1	211 2.	10178.32	2385.71	4.27 0.23 2.09
1_2_21_22 E7450			15610.84	3692.83	4.23 0.24 2.08
4_4_13_13 E2084	4587610 (AC006951) putative indole-3-glycerol phosphat...+2	413 €	9299.15	2244.55	4.14 0.24 2.05
1_2_14_2 E1909			21686.4	5464.56	3.97 0.25 1.99
2_3_12_21 E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR I		9856.65	2493.14	3.95 0.25 1.98
2_4_20_5 E1562	3164138 (D78604) cytochrome p450 monooxygenase [Arabid...+3	3	10802.32	2744.4	3.94 0.25 1.98
1_4_14_7 E1962			23965.51	6123.9	3.91 0.26 1.97
1_4_21_5 E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2	380	10472.11	2679.08	3.91 0.26 1.97
2_3_10_20 E2884			4262.66	1094.31	3.9 0.26 1.96
1_3_7_19 E4493	G626		2226.28	576.05	3.86 0.26 1.95
3_1_7_14 E4413	G29		1936.76	511.28	3.79 0.26 1.92

4_1_5_6	E6700	2827546 (AL021635) cytochrome P450 like protein [Arabi...+2	853	18637.8	4979.11	0.27	1.9
2_4_18_9	E3822	3193296 (AF069298) similar to pectinesterase [Arabidop...+3	700	1	3429.65	922.82	3.72
3_1_20_12	E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana]	+2	727	4.	22361.9	6019.52
1_2_21_12	E1843				6645.83	1795.4	3.7
1_4_15_13	E2354				3257.25	881.63	0.27
2_4_7_22	E4570	G1043			309.2	250.02	3.64
2_2_14_3	E2103	3021273 (AL022347) serine/threonine kinase - like prot...+2	543	1.3	1471.6	405.15	3.63
3_1_19_11	E3922	1086263 TMV resistance protein N - tobacco (Nicotiana ...+3	262	1.	3114.44	864.4	3.6
2_4_13_16	E2126				2969.76	830.85	3.57
2_4_7_13	E4408	G350			2726.62	768.74	3.55
2_4_14_2	E2102	4512651 (AC007048) putative tyrosine transaminase [Ara...+2	648	!	2397.45	3.55	0.28
1_4_16_7	E2990				3674.18	1037.57	3.54
3_1_21_14	E1865	3367517 (AC004392) Similar to F411.26 putative beta-gl...+2	697	6.	3209.07	917.98	3.5
1_4_10_21	E2697	3738287 (AC005309) glutathione s-transferase, GST6 [Ar...+2	680		6208.81	1841.93	3.37
1_4_1_1	E4001				436.47	130.05	3.36
1_1_12_16	E538				14828.76	4443.63	3.34
2_2_7_19	E4515	G1004			957.42	286.35	3.34
2_4_9_18	E7385	G1468			8179.27	2461.52	3.32
3_4_19_16	E1056	4559358 (AC006585) putative steroid binding protein [A...+3	203	1.	9811.91	2973.44	3.3
1_3_17_6	E3172	1170089 GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >F			15815.37	4827.44	3.28
3_1_9_20	E5095	G515			504.42	153.57	3.28
3_2_21_21	E7460				7271.88	2230.11	3.26
2_3_21_8	E1758	2129600 glutathione synthase (EC 6.3.2.3) 2 - Arabidop...+2	441	8.	6460.75	2011.94	3.21
3_4_11_20	E2269				10588.89	3295.03	3.21
2_2_13_15	E2081	4680337 (AF128457) hypothetical protein [Oryza sativa ...+1	234	1.	7588.93	2375.2	3.2
2_3_1_19	E4069				7206.52	2284.74	3.15
3_2_21_4	E1725	caffeic o-methyltransferase			2228.88	730.72	3.05
2_3_10_10	ECE2822	112785 DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLAD			2390.11	3.04	0.33
2_4_16_21	E2822	112785 DNA-3-METHYLADENINE GLYCOSIDASE II (3-METHYLAD			9056.4	2988.64	3.03
1_2_10_15	E2684				9656.22	3205.93	3.01
1_2_22_2	E7456				6189.7	2071.78	2.99
4_4_13_14	E2086				11985.51	4004.9	2.99
3_4_13_17	E1942	2832663 (AL021710) hypothetical protein [Arabidopsis t...+2	239	2.	15793.4	5294.33	2.98
2_4_7_16	E4457	G195			855.5	291.3	2.94
2_3_14_20	E2367	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECUR			5505.02	1890.07	2.91
2_4_12_7	E432				10416.78	3582.26	2.91
1_3_19_2	E3857	3776578 (AC005388) ESTs 9b F13915 and gb F13916 come f...+2			11930.52	4122.97	2.89
							0.35
							1.53

1_2_8_2	E4591	G263	5048.8	1752.24	2.88	0.35
2_2_13_15	E2089	14043.16	4911.1	2.86	0.35	1.52
3_2_21_22	E7462	8363.31	2920.2	2.86	0.35	1.52
1_3_16_1	E2789	9599.7	3369.53	2.85	0.35	1.51
1_1_12_13	E491	10421.53	3647.67	2.84	0.35	1.5
1_3_14_22	E2190	10421.53	3671.11	2.84	0.35	1.51
2_4_13_15	E2090	2827714 (AL021684) receptor protein kinase - like prot... +1	191 2.2	8107.14	2856.98	0.35
3_1_10_14	E2501	4540.27	1598.18	2.84	0.35	1.51
4_1_13_17	E2037	3395425 (AC004683) putative DNA binding protein [Arabidopsis thaliana] +1 526 :	20183.55	7106.8	2.84	0.35
4_3_9_1	E4918	3840.26	1352.87	2.84	0.35	1.51
2_4_1_19	E4069	7834.14	2769.97	2.83	0.35	1.5
3_2_20_13	E1391	2739389 (AC002505) Cf-2.2 like protein [Arabidopsis thaliana] +1 574 2.1	9871.88	3484.18	2.83	0.35
1_4_20_8	E1335	8704.06	3085.78	2.82	0.35	1.5
1_1_7_16	E4431	G515	652.35	231.77	2.81	0.36
1_1_10_16	E2457	4328.43	1540.03	2.81	0.36	1.49
4_4_10_13	E65	8403.75	3004.34	2.8	0.36	1.48
1_1_21_22	E7171	2555.2	917.19	2.79	0.36	1.48
2_2_20_22	E1615	3451070 (AL031326) putative protein [Arabidopsis thaliana] +1 256 3.3	9271.68	3340.58	2.78	0.36
1_1_20_11	E1287	G742	6776.9	2444.55	2.77	0.36
2_2_3_8	E6027	3123296 CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED :	14596.44	5261.67	2.77	0.36
2_4_12_12	C E792	G1202	10617.88	3836.85	2.77	0.36
1_4_20_21	E1606	3341698 (AC003672) blue copper-binding protein II [Arabidopsis thaliana] +2 421 2.	7755.57	2814.22	2.76	0.36
1_2_17_4	E3372	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +2 574 6	7801.38	2844.96	2.74	0.36
3_1_11_6	E2489	16729.45	6117.75	2.73	0.37	1.45
2_1_16_8	E3123	13751.41	5062.33	2.72	0.37	1.44
3_3_10_15	E2512	5868	2154.79	2.72	0.37	1.45
1_1_12_18	E501	4115383 (AC005967) receptor-like protein kinase [Arabidopsis thaliana] +1 180 6.	5030.98	1865.8	2.7	0.37
1_1_13_17	E921	13821.58	5160.8	2.68	0.37	1.42
2_1_14_9	E2019	16949.48	6331.86	2.68	0.37	1.42
4_4_15_13	E2629	9408.09	3519.15	2.67	0.37	1.42
2_3_20_11	C E1434	2832642 (AL021710) putative protein [Arabidopsis thaliana] +1 493 1.4	6069.11	2282.63	2.66	0.38
3_4_11_8	E2723	4689448 (AC006267) putative xylan endohydrolase [Arabidopsis thaliana] +3 177	5846.02	2204.28	2.65	0.38
4_2_13_5	E855	3608412 (AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum] +2 46	11639.43	4394.41	2.65	0.38
4_4_20_17	E1592	14563.79	5505.94	2.65	0.38	1.4
1_4_1_6	E4011	14212.87	5378.23	2.64	0.38	1.4
1_4_1_19	E4069	11812.95	4474.21	2.64	0.38	1.4
2_3_13_1C	E764	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +1 171 3	4155.98	1572.92	2.64	0.38
gst6						
caffic o-methyltransferase						

1_3_15_22 E2743	3152621 (AC004482) cold acclimation protein WCOR413-[l... +2 491	9846.11	3762.33	1.39
2_3_15_9 E2391	2252854 (AF013294) similar to auxin-induced protein [A....+1 190 3.	8564.9	3285.36	0.38
3_3_9_9 E5076	G28	5392.72	2068.28	2.61
4_1_8_2 E4611	G5555	913.84	350.29	2.61
1_1_12_12 E489		6846.79	2636.96	2.6
1_2_13_21 E1901		9420.8	3630.3	2.6
1_3_1_19 E4069	caffeo o-methyltransferase	10995.37	4221.25	2.6
2_4_14_14 E2542	3434969 (AB008104) ethylene responsive element binding... +2 422	7289.2	2806.68	0.38
1_1_12_23 E552		114117.89	4402.5	2.59
1_3_9_4 E4737	G271	3427.1	1323.33	2.59
1_1_14_5 E943		11001.57	4257.53	2.58
1_2_9_1 E4844	G1006	41117.54	1605.18	2.57
1_3_21_4 E1696	2262100 (AC002343) unknown protein [Arabidopsis thaliana] +1 429	10141.27	3942.7	2.57
1_3_10_18 E2462	1208408 (D14824) nitrite reductase [Arabidopsis thalia... +3 137 1.6.	3732.49	1459.32	2.56
1_4_10_12 E2637	2651316 (AC002336) unknown protein [Arabidopsis thaliana] -2 113	3817.08	1492.45	2.56
3_1_10_17 E2465		8455.27	3307.84	2.56
3_1_21_7 E1767		12958.61	5066.78	2.56
1_4_21_23 E7453		58117.12	2279.87	2.55
1_3_11_8 E2530		5030.97	1984.43	2.54
1_1_16_5 E2754	2980766 (AL022198) putative calmodulin-binding protein... +2 491 4	8791.1	3470.21	2.53
4_1_10_11 E2829	4567201 (AC007168) putative aspartate aminotransferase... +1 109	1364.43	540.17	2.53
4_4_14_17 E2595	4206196 (AF071527) hypothetical protein [Arabidopsis t... +2 272 5.	7667.19	3034.14	2.53
1_3_21_13 E1840	1171991 PHENYLALANINE AMMONIA-LYASE 1>pir S529990 phe... .	16934.48	6729.96	2.52
1_4_12_11 E290		15016.19	5987.17	2.51
1_2_3_23 E5917	2062169 (AC001645) ABC transporter (PDR5-like) isolog ... +1 237	41166.34	16441.5	2.5
1_3_10_14 E2496	2497753 NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSO	5431.44	2169.62	2.5
3_1_10_15 E2503	510876 (X80051) NADP dependent malic enzyme [Phaseolu... +1 1	6324.08	2526.8	2.5
3_2_22_1 E0		466.9	186.46	2.5
1_4_19_12 E1042	2924785 (AC002334) similar to disease resistance prote... +2 250 1	1849.62	744.09	2.49
3_4_11_6 E2677		11264.39	4530.91	2.49
2_1_2_18 E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1 561 8	17043.36	6870.23	2.48
3_1_11_5 E2487	3915085 TRANS-CINNAMATE 4-MONOXYGENASE (CINNAMIC A	8504.09	3426.41	2.48
1_2_14_22 E2285	1363482 IAA11 protein - Arabidopsis thaliana >gi 97292... +3 434 4.	7643.69	3097.61	2.47
2_1_17_17 E3682	115486 CALMODULIN-2/3/5 >pir S22503 calmodulin - Ara... +2 592	14519	5873.99	2.47
2_4_7_17 E4454	G187	1205.55	487.74	2.47
4_2_10_16 E28		7421.43	3010.28	2.47
1_3_15_23 E2745		8461.8	3440.08	2.46

1_2_15_15_E2967	2160190 (AC000132) No definition line found [Arabidops...]	+2	455	2	9954.85	4064.31		
1_4_16_3_E2982	2584721 (Y10157) sulfite reductase [Arabidopsis thaliana] +1	497	2.	26468.04	10802.41	2.45	0.41	1.29
1_3_9_13_E5069	G189			10259.39	4196.51	2.44	0.41	1.29
2_3_21_7_E1756	G22			1420.49	583.36	2.44	0.41	1.28
2_4_13_13_E2078	g130333375 putative berberine bridge enzyme from Arabidopsis thaliana			15568.05	6418.88	2.43	0.41	1.28
4_1_11_14_E351	2924777 (AC002334) putative receptor protein kinase [A...]	+2	116	2	9719.27	4006.79	2.43	0.41
4_1_14_5_E2059	3850571 (AC005278) Similar to gblU85207 snRNP core Sm ...	+2	35	10033.66	4146.96	2.42	0.41	1.27
2_2_15_22_E3027	3766368 (AL031907) putative transcription factor, ccr4... +1	157	3.7e	9031.76	3736.72	2.42	0.41	1.27
2_3_20_16_E1446	3367524 (AC004392) F8K4.12 [Arabidopsis thaliana]	+3	284	3.	8302.41	3450.52	2.41	0.42
3_1_19_18_E3936	3164138 (D78604) cytochrome p450 monooxygenase [Arabid...]	+2	7	9774.11	4050.3	2.41	0.41	1.27
1_1_12_2C_E505	4218011 (AC006135) putative protein kinase [Arabidopsi...]	+2	378	1	5397.13	2249.36	2.4	0.42
2_2_2_11_E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabid...]	+2	7	9774.11	4050.3	2.41	0.41	1.27
1_1_12_14_E493	4218011 (AC006135) putative protein kinase [Arabidopsi...]	+2	378	1	5397.13	2249.36	2.4	0.42
1_1_16_8_E1796				8385.09	3498.53	2.4	0.42	1.26
2_1_13_1C_E763				5108.43	2132.61	2.4	0.42	1.26
4_4_10_11_E19	G1145			7179.61	2992.49	2.4	0.42	1.26
1_1_19_23_E1265	1703220 AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabid...]	+2	5	9661.9	4037.36	2.39	0.42	1.26
1_2_12_16_E634	4583153 (AF108211) cytosolic inorganic pyrophosphatase... +1	243		13267.86	5557.51	2.39	0.42	1.26
1_4_11_17_E215	23522828 (AF0092228) NaCl-inducible Ca2+-binding protein... +3	518		6871.98	2874.02	2.39	0.42	1.26
2_2_19_1C_E1191				7669.07	3214.05	2.39	0.42	1.25
4_2_12_2C_E797				5589.18	2337.69	2.39	0.42	1.26
4_2_16_4_E7102	G619			2027.69	847.01	2.39	0.42	1.26
4_4_13_18_E2096	2440035 (X98544) endo-1,4-beta-glucanase [Arabidopsis ...]	+2	743	13570.65	5668.97	2.39	0.42	1.26
2_1_15_12_E2433				8196.36	3445.65	2.38	0.42	1.25
2_4_17_13_E2884				3734.31	1566.63	2.38	0.42	1.25
2_4_21_18_E3296	2781394 (U70424) O-methyltransferase 1 [Arabidopsis th...]	+3	325	9323.53	3922.33	2.38	0.42	1.25
3_1_21_1_E1671	4006918 (Z99708) peroxidase like protein [Arabidopsis ...]	+2	700	3.(6719.76	2826.5	2.38	0.42
1_1_8_23_E4765	G620			234.26	98.88	2.37	0.42	1.24
2_4_14_15_E2544				7301.69	3086.91	2.37	0.42	1.24
2_4_20_6_E1564	3434967 (AB008103) ethylene responsive element binding...	+1	272	7292.96	3078.58	2.37	0.42	1.24
3_4_11_5_E2675	1076211 hypothetical protein VSP-3 - Chlamydomonas rei... +2	184		8982.65	3783.32	2.37	0.42	1.25
3_2_8_23_E4855	G1383			3817.16	1617.13	2.36	0.42	1.24
1_1_15_6_E2245	1706917 FLAVONOL SULFOTRANSFERASE-LIKE >pir S69188 fl...			6547.54	2787.07	2.35	0.43	1.23
1_1_19_17_E3928	4263771 (AC006218) putative nonspecific lipid-transfer... +1	491	4.2	5274.81	2243.56	2.35	0.43	1.23
1_2_20_22_E1607	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +2	663		3920.89	1665.6	2.35	0.42	1.24
2_4_13_23_E2140				7926.91	3369.18	2.35	0.43	1.23
3_3_13_17_E928				10353.41	4409.1	2.35	0.43	1.23

EXHIBIT F

EID	COMMENT	(0.944)CY5	CY5	CY5/(0.944)CY3 SOURCE
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (F	543.622	38569.4	70.949 L20P15F02,L35P91G09
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida]	+2 384 :	573.554	31.651 L17P17D04,L35P107H01
E2050			1336.744	26.296 L20P13A01,L35P91D10
E3171	481821 probable glutathione transferase (EC 2.5.1.18)...+3 586 :	1595.128	36546.61	22.911 L15P4C09,L35P101E03
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis th...+1 581	817.426	9283.46	11.357 L18P29E04,L35P88H06
E5077	G354		437.549	10.591 J129B10F1
E4591	G263		656.994	10.203 J124B01F1
E2049	3851530 (AF065435) nodulin [Glycine max]	+3 640 6.8:	2295.556	10.147 L20P12H08,L35P91D09
E1197			23292.02	10.005 L18P10G01,L35P112F07
E2684			650.772	9.201 L15P8B11,L35P78A11
E4107	GP-39		1240.547	
E4407	G353		11414.5	
E1374	4725948 (AL049730) putative Phospholipase D [Arabidopsis thaliana] +3 3{:	247.063	24625.66	8.773 O17201,M80927
E4794	G915		2807.056	8.72 J122D01F1
E1200	2829919 (AC002291) Unknown protein [Arabidopsis thaliana] +3 2	615.534	5037.75	8.184 L18P33H09,L35P114C12
E4111	GP-39		937.549	8.177 J126D04F1
E1832			7666.25	8.003 L18P10H11,L35P112F10
E2109	2052383 (U666345) calreticulin [Arabidopsis thaliana]	+1 477 1:.	710.493	7.604 O17205,M80927
E2126	G348		3787.444	7.169 L28P4E07,L35P119H02
E4570	G1043		2748.09	7.017 L20P2H03,L35P92F03
E3173	3241945 (AC004625) unknown protein [Arabidopsis thaliana] +2 3{:	5429.877	2880.72	6.832 L20P17D07,L35P92A08
E2111	2739381 (AC002505) putative patatin [Arabidopsis thali...+2 353	38102.85		
E6736	3851530 (AF065435) nodulin [Glycine max]	+2 408 2.6{:	2589.263	
E4610	G503		1669.306	
E501	4115383 (AC005967) receptor-like protein kinase [Arabi...+1 180	1469.642	17690.62	
E4109	GP-39		38102.85	
E1460	3451056 (AL031326) serine/threonine kinase - like prot...+1 196 :	3904.479	11210.13	
E3727	3036808 (AL022373) DmaJ-like protein [Arabidopsis thal...+2 501	2243.568	9650.99	6.137 L17P32C01,L35P85C01
E1949	4539301 (AL049480) putative mitochondrial protein [Ara...+2 280	1708.963	25296.03	6.121 O17203,M80927
E4918	G348		569.135	6.102 L18P8F11,L35P115B08
E3736	1695719 (D89342) luminal binding protein [Arabidopsis th...+1 773	523.482	3662.91	5.941 L17P15D06,L35P107B10
E1525	2160152 (AC000375) ESTs gb U75592,gb T13956,gb T43869 ...+2	555.878	3455.08	5.863 L18P4E04,L35P90C11
E4664	G553		3133.282	5.518 J127F10F1
E1559	2244869 (Z97337) hypothetical protein [Arabidopsis tha...+2 356	1487.875	2888.43	5.376 L17P16D02,L35P107D08
E2788	1523796 (X97864) cytochrome P450 [Arabidopsis thaliana] +1 29	2259.751	1100.709	5.33 L20P7B02,L35P116E01
E4844	G1006		742.606	5.309 J124F11F1
			2259.751	5.194 L20P2E02,L35P116B11
			11734.11	5.193 L23P5G04,L35P97C07
			780.45	5.176 J126E09F1
			4039.75	

E4630	G19		1624.861	8339.05	5.132	J124B10F1
E6869		720.814	3617.95	5.019	J47G05F1	
E1235		1960.756	9778.73	4.987	L18P27D06,L35P113D03	
E1909		4884.253	24309.01	4.977	L18P5C02,L35P90E01	
E1454	3688186 (AL031804) putative protein [Arabidopsis thaliana] +3	676 1	2203.476	10854.56	4.926	L18P6F12,L35P115A08
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thaliana	+3 493 2	2005.276	9863.7	4.919	L17P27B07,L35P109H01
E1491	3193289 (AF069298) similar to several small proteins (... +1	415 4	2260.233	10986.97	4.861	L20P16E07,L35P115G09
E1424	2224933 (AF004216) ethylene-insensitive3 [Arabidopsis thaliana] +2	486	1275.625	6183.14	4.847	L20P11E03,L35P115D02
E4586	G1427		342.165	1649.61	4.821	J123H08F1
E4444	G371		414.709	1998.31	4.819	J122C09F1
E5067		627.912	2947.53	4.694	J129A09F1	
E1450	2914705 (AC003974) putative disease resistance protein... +1	285	716.536	3349.54	4.675	L20P17C01,L35P115H04
E567			1732.19	8081.93	4.666	L17P37H03,L35P85F08
E1867	2435406 (U83490) thaumatin-like protein [Arabidopsis thaliana]	+2 573	996.241	4568.44	4.586	L28P1F06,L35P119F07
E1209	1495269 (X97829) product similar to ccr protein, Citrus...	+1 387 1	1892.716	8257.91	4.363	L18P17E02,L35P112H07
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat...	+2 413	3302.844	14378.33	4.353	L20P17H02,L35P92B02
E2086			2913.592	12600.34	4.325	L20P1A01,L35P92B04
E4827	G186		230.662	991.04	4.296	J126C05F1
E2990		3159.116	13532.76	4.284	L28P3C02,L35P98E08	
E5030	G789	1248.951	5339.89	4.276	J128D10F1	
E4014	CATALASE 3	1407.248	5975.97	4.247	L15P9C05F1	
E1211	4455208 (AL035440) putative protein [Arabidopsis thaliana] +2	486 1	1752.529	7401.57	4.223	L18P17G07,L35P112H09
E1080			2335.298	9794.7	4.194	L17P41F08,L35P111D04
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]	+3 7	2149.533	9003.91	4.189	L17P16C08,L35P107D06
E617		2	1230.038	5111.19	4.155	L17P6D01,L35P86F04
E6768		1600.453	6642.4	4.15	J46F06F1	
E1289	2281631 (AF003096) G19 AP2 domain containing protein RAP2....		3059.227	12668.69	4.141	L18P29A07,L35P113E09
E4108	GP-39	598.122	2457.8	4.109	O17202,M80927	
E2551		4274.989	17375.04	4.064	L22P8E01,L35P96B05	
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana	+3 840 :	2836.449	11520.22	4.061	J129B06F1
E4675	G629	697.491	2810.87	4.03	J124H05F1	
E1546		658.495	2650.28	4.025	L21P9B05,L35P116H04	
E1456	1172599 PROTEASOME COMPONENT C5 (MULTICATALYTIC ENZYME)		1054.811	4228.73	4.009	L18P6H10,L35P115A10
E1769	871782 (L43081) pEARLI 4 gene product [Arabidopsis thaliana] +2	57C	895.597	3590.37	4.009	L23P12E04,L35P118E11
E2251		1912.913	7652.44	4	L22P11C08,L35P93F07	
E3416		1716.318	6859.17	3.996	L15P9B06,L35P103C04	
E76	4677328 (AL049658) aldehyde dehydrogenase (NAD+)-like ... +2 :		3385.029	13472.7	3.98	L16P7G07,L35P80D07

E2682	3702964 (AF079485) rac GTP binding protein Arac10 [Ara... +1 49	1914.858	7589.12
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1 293 z	1255.343	4933.99
E1011	4263818 (AC006067) unknown protein [Arabidopsis thaliana] +3 1{	1334.817	5245.54
E2743	3152621 (AC004482) cold acclimation protein WCOR413-li... +2 4{	1367.015	5334.48
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2 3{	1605.344	6260.1
E2037	3395425 G915 (AC004683) putative DNA binding protein [Arabi... +	4678.14	18204.85
E1847	G899.	2225.184	8566.58
E3296	2781394 (U70424) O-methyltransferase 1 [Arabidopsis th... +3 325	1894.076	7254.63
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3 185 1	1924.593	7236.45
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3 462	1107.318	4154.28
E3531	3168840 (U88711) copper homeostasis factor [Arabidopsi... +1 54{	2883.33	10769.87
E4014	CATALASE 3	1834.619	6839.57
E1455	128188 NITRATE REDUCTASE 2 (NR2) >pir IRDMUNH nitrate ... +	4747.021	17496.84
E2737	4115914 (AF118222) contains similarity to Iron/Ascorbate family of {	2668.747	9816.58
E4575	G1275	425.378	1554.78
E1843		2260.903	8233.04
E3579	1705677 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >pir S.	3195.846	11578.25
E146	1361986(G364) finger protein 2 - Arabidopsis thaliana >gi 79...+1	846.224	3058.56
E2547	3047119 (AF058919) No definition line found [Arabidops... +2 727	1762.811	6332.48
E4349	G921	1639.61	5889.22
E4659	G511	1084.072	3890.93
E3261	2894599 (AL021889) putative protein [Arabidopsis thali... +1 587 z	3872.867	13888.17
E2977	3341679 (AC003672) dynamin-like protein phragmoplastin... +1 26	2543.148	9070.67
E5027	G528	3620.223	12858.98
E2807		813.658	2888.7
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 calnexin	2199.992	7778.4
E3084		2668.719	9430.95
E3570		6848.899	24180.65
E2805		1883.199	6610.18
E3702	3297815 (AL031032) putative protein [Arabidopsis thali... +1 219 z	1897.239	6642.75
E1465		1369.385	4790.79
E1472	1707013 (U78721) Brassica napus hypothetical protein 2... +3 346	1162.838	4058.27
E1106	2129634 lectin-like protein - Arabidopsis thaliana >em... +1 426 3.	4574.824	15918.3
E308	2828292 (AL021687) neoxanthin cleavage enzyme-like pro... +3 1{	1140.677	3961.46
E4839	4544394 (AC007047) hypothetical protein [Arabidopsis t... +3 631	670.619	2315.81
E1537	3777449 (AJ011844) ppc2 [Solanum tuberosum]	+1 433 :	1762.811
E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana]	+3 491 :	1136.353
			3900.41

E3829	4507433 testis enhanced gene transcript >sp P55061 TEG... +3	1€	8167.193	27999.71	3.428 L17P1G02,L35P108F09
E1155	4531445 (AC006224) unknown protein [Arabidopsis thaliana] +3	5{	819.597	2808.55	3.427 L18P10D05,L35P112F01
E3554	4185509 (AF102821) actin depolymerizing factor 3 [Arab... +3	637	3894.952	13335.28	3.424 L16P5E08,L35P105E05
E3463	3123188 CATALASE 3 >gi 2347178 (U43147) catalase 3 [Ar... +2	.	10783.952	36889.66	3.421 L15P9C05,L35P103C09
E6297	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +2	24{	1003.134	3426.68	3.416 J39G07F1
E4758	G899		325.782	1111.97	3.413 J125C08F1
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (N		2836.204	9654.93	3.404 L18P7C03,L35P115A12
E2979	2191147 (AF007269) A_IG002N0126 gene product [Arabido... +1		3705.665	12564.45	3.391 L28P1E05,L35P98C09
E2382	2213626 (AC000103) F21J9.18 [Arabidopsis thaliana]	+2	468	1547.983	3.379 L22P3G11,L35P95E05
E1593				1443.978	3.373 L22P10A10,L35P116H09
E2309				4869.88	3.356 L22P21D08,L35P94G05
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC IS		2710.916	9096.95	3.332 L20P14B07,L35P91E10
E4465	G5		1862.775	6206.1	3.314 J122E08F1
E5114	G915		1072.76	3554.76	3.302 J129G01F1
E4519	G1009		1379.932	4557.12	3.298 J123D03F1
E3685	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi... +3	3	475.223	1567.52	3.284 L17P14A11,L35P107A04
E3285	3805847 (AL031986) putative protein [Arabidopsis thali... +1	246	1643.632	5397.49	3.28 L34P1D11,L35P120B09
E4663	G525		1305.509	4281.8	3.275 J124F07F1
E2533			649.667	2127.73	
E6225	3075398 (AC004484) unknown protein [Arabidopsis thaliana] +3	7:	559.523	1823.36	3.259 L15P7B11,L35P77G11
E2059	2924777 (AC002334) putative receptor protein kinase [A... +2	116	1000.008	3255.42	3.255 J39D01F1
E1287	4587989 (AF085279) hypothetical Cys-3-His zinc finger ... +3	255	3441.691	11162.86	3.243 L20P14E08,L35P91F07
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara... +2	33{	5228.419	16951.09	3.242 L18P28C09,L35P113E07
E3420	4689436 (AF143096) peptidyl-prolyl-cis-trans isomerase... +3	224	1414.934	4575.24	3.234 L22P10B04,L35P116H10
E4905	G6		2522.441	8136.57	3.226 L15P9E08,L35P103D02
E4514	G986		2092.295	6748.6	3.225 J127D04F1
E1985			228.387	736.52	3.225 J123C12F1
E2968			660.27	2127.74	3.223 L18P8F06,L35P91A05
E3726	3249099 (AC003114) EST gb T21244 comes from this gene... +2		3470.414	11167.18	3.218 L24P5H11,L35P98A10
E3922	1086263 TMV resistance protein N - tobacco (Nicotiana ... +3	262	1495.23	4798.31	3.209 L17P15D01,L35P107B09
E1428	1946371 (U93215) regulatory protein Viviparous-1 isolo... +3	299	921.28	2949.03	3.201 L17P25H03,L35P109F09
E3468	G654		1569.238	4957.17	3.159 L20P11G03,L35P115D06
E1348	3021270 (AL022347) serine/threonine kinase -like prote... +3	662	1869.904	5903.25	3.157 L15P9G04,L35P103D08
E3240	1707011 (U78721) auxin-repressed protein isolog [Arabi... +3	529	1978.555	6236.2	3.152 L18P4H10,L35P114G03
E5069	G189		5770.342	18128.96	3.142 L15P5A11,L35P101H12
E3344	2760324 (AC002130) F1N21.9 [Arabidopsis thaliana]	+3	909.864	2853.61	3.136 J129A10F1
E670	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2	6:	776	559.957	3.136 L17P7G08,L35P102G01
				1756.11	3.135 L17P7B05,L35P86G09
				6571.1	

E11265	1703220 AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabid... +2	2627.41	8225.68
E22428	2191140 (AF007269) contains weak similarity to MYB-rel... +2	440	1330.285
E4377	G528	1631.31	5079.38
E4518	G1050	743.748	2314.46
E1871		1370.971	4245.3
E4635	G209	365.817	1129.86
E5031	G895	1119.433	3447.93
E1714		1495.523	4599.98
E2578	4455220 (AL035440) putative aconitase [Arabidopsis tha... +3	194	2510.27
E3748	4324714 (AF110771) ammonium transporter [Arabidopsis t... +1	3	7739.662
E4405	G427	1407.645	23646
E2378		3058.066	4299.92
E764	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +1	171	3570.425
E1796		10865.12	9334.48
E6637	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +3	698	1712.654
E4450	G354	1255.315	5200.44
E2099		375.221	3811.66
E2546	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3	6	2116.155
E2137	3164222 (AB008518) RMA1 [Arabidopsis thaliana] >gi 420... +1	41	6408.84
E6877	1352347 ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >pir ...		3555.06
E4666	G554	12630.59	38191.51
E680		1953.354	5889.43
E1555	2914703 (AC003974) unknown protein [Arabidopsis thaliana] +3	41	409.468
E1237		409.468	1229.85
E3734		569.229	1707.68
E250	2618727 (U49075) IAA19 [Arabidopsis thaliana] +2	334	5743.43
E3886	2642215 (AF030386) NOI protein [Arabidopsis thaliana] +1	298	569.229
E2139	4249410 (AC006072) unknown protein [Arabidopsis thaliana] +1	3	12034.73
E1807	4741198 (AL049746) putative protein [Arabidopsis thali... +2	467	3276.623
E4537	G1273	1978.772	9805.89
E1583	3695023 (AF055850) unknown [Arabidopsis thaliana] +2	502	1978.772
E4797	G1216	127.365	4458.27
E3729	3702339 (AC005397) unknown protein [Arabidopsis thaliana] +2	1	127.365
E2387	2191176 (AF007270) Similar to SRF-type transcription f... +3	282	3473.87
E4560	G787	1821.522	10350.6
E1992		479.604	5894.73
E1414	4263710 (AC006223) putative pur-alpha transcriptional ... +3	528	5360.25
			1408.03
			2558.586
			7489.53
			6994.71
			2391.809

A408-Methylamine-24 hrs

EXHIBIT G

EID	COMMENT	(0.928)CY:CY5	CY5/(0.928 METAROW METACOL ROW
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3	396	1139.28 16921.29 14.853 2 4 10
E4218		605.059	4711.85 7.787 3 2 22
E5356	3319350 (AF077407) No definition line found [Arabidops... +3	894	5519.182 29171.3 5.285 3 1 2
E6937	3319350 (AF077407) No definition line found [Arabidops... +3	539	5679.418 28673.45 5.049 1 1 1 7
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana]	+3	330 1 6094.503 27977.94 4.591 3 2 9
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2	42{	9535.867 42891.9 4.498 3 3 3 12
E808	2832649 (AL021710) adenylosuccinate lyase - like prote... +2	250	3831.85 16777.87 4.379 4 4 4 10
E2202	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQz		2046.401 8782.5 4.292 1 3 3 12
E986	A.thaliana beta tubulin 1		6062.818 25668.52 4.234 3 2 2 16
E4143		766.279	3129.92 4.085 2 3 3 22
E132		1292.022	5276.57 4.084 1 1 1 9
E436		1632.976	6441.13 3.944 4 4 4 9
E3566	4117381 NITRILASE 1 >pir S22398 nitrilase (EC 3.5.5.1... +2	530	: 13738.8 52724.44 3.838 1 1 1 15
E4145	A.thaliana beta tubulin 1		1470.04 5596.3 3.807 2 3 3 22
E5358		2935.026	11149.61 3.799 3 2 2 22
E4220	G222	775.221	2928.52 3.778 3 2 2 22
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2	564	10473.74 39443.37 3.766 2 2 2 14
E4147	A.thaliana beta tubulin 1		516.199 1918.98 3.718 2 2 3 22
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQz		1589.158 5691.49 3.581 4 2 2 4
E6415	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQz		2407.937 8535.44 3.545 4 4 4 4
E6978	3319350 (AF077407) No definition line found [Arabidops... +2	553	: 4906.785 17354.87 3.537 3 3 4 7
E4227		619.854	2048.93 3.306 3 2 2 9
E234	4468813 (AL035601) putative protein [Arabidopsis thali... +3	555 1.	4160.56 13698.29 3.292 3 2 2 9
E2649	3785997 (AC005499) putative annexin [Arabidopsis thali... +1	595	1145.217 3765.91 3.288 1 4 7
E4217	G40	265.163	843.82 3.182 1 4 2 22
E4267	G256	566.64	1794.82 3.167 3 2 2 22
E4603	G451	1116.462	3440.91 3.082 2 2 2 20
E2167	4455154 (AL033545) extensin - like protein [Arabidopsi... +2	394 2.	1881.489 5750.38 3.056 4 2 2 22
E4357	G921		948.972 2895.86 3.052 3 1 20
E157	2460203 (AF021244) coronatine-induced protein 1 [Arabi... +2	247	2388.718 7165.85 3 1 3 8
E4222		785.526	2349.92 2.992 1 1 2 22
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1	293 2.	4302.617 12507.62 2.907 1 3 17
E540	4587542 (AC006577) Belongs to the PF 00657 Lipase/Acyl... +3	37	6999.601 20120.82 2.875 1 1 1 9
E4274		959.008	2699.26 2.815 1 2 2 22
E3334	3319347 (AF077407) No definition line found [Arabidops... +2	447	: 12896.57 35989.06 2.791 1 2 14
E1783	4589123 (AF126374) At14a protein [Arabidopsis thaliana]	+1	566 1670.19 4516.59 2.704 3 2 19

E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	4312.532	11412.41	2.646
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1	43: 5050.771	13249	2.623
E5430		3574.414	9288.17	2.599
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S66354 ...	4667.409	12121.77	2.597
E5935		2967.88	7639.68	2.574
E6215	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMM)	4668.772	11954.27	2.56
E5632	2062161 (AC001645) jasmonate inducible protein isolog ...+2	3558.024	9022.69	2.536
E2656	261 (AC001645) jasmonate inducible protein isolog ...+2	12343.26	31282.46	2.534
E6980		3561.289	8983.47	2.523
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3166.972	7965.66	2.515
E6973		2406.546	6047.09	2.513
E4540	G1356	1045.123	2619.77	2.507
E6578	2244888 (Z97338) similarity to cytochrome P450 [Arabid...+2	2870.309	7170.28	2.498
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3 396 :	1478.472	3629.11
E6417		2219.985	5444.37	2.452
E159		2672.868	6521.4	2.44
E370		350.109	848.86	2.425
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara...+2	335 2083.318	5008	2.404
E1493	2062164 (AC001645) jasmonate inducible protein isolog ...+1	555 10793.82	25838.11	2.394
E2232	2924509 (AL022023) subtilisin proteinase - like [Arabi...+3	277 7.5	7939.706	18747.73
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-...+1	52: 4180.419	9862.21	2.359
E4257	G210	664.256	1542.93	2.323
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR	8653.151	20097.13	2.323
E3397	4580920 (AF113545) vacuole-associated annexin VCaB42 [...+1	3: 5872.073	13557.76	2.309
E4272	G412	397.248	916.71	2.308
E3115		19656.46	45319.03	2.306
E2472		4924.585	11320.4	2.299
E5592		1941.892	4448.39	2.291
E6535	2129516 1-aminocyclopropane-1-carboxylate oxidase homo...+2	1: 1015.543	2320.32	2.285
E5432	3193290 (AF069298) contains similarity to a protein ki...+1	415 7.0	1887.685	4282.93
E6340		1764.57	3978.9	2.255
E3332	2062161 (AC001645) jasmonate inducible protein isolog ...+1	671 18236.58	41042.81	2.251
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3828.464	8588.66	2.243
E1999		5222.871	11707.85	2.242
E5708	3885331 (AC005623) putative cytochrome p450 protein [A...+2	26: 4947.283	11073.51	2.238
E1693	4468807 (AL035601) cytochrome P450 monooxygenase-like ...+3	: 7253.346	16025.03	2.209
E6943	2642444 (AC002391) putative cytochrome P450 [Arabidops...+2	5: 1268.555	2799.08	2.207

E3920	4115377 (AC005967) unknown protein [Arabidopsis thaliana] +1 26	4558.216	10061.95	2.207	16
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1 561	3697.168	8108.17	2.193	2
E6255	2244889 (Z97338) similarity to cytochrome P450 [Arabid... +3 228	1645.61	3606.27	2.191	3
E4767	G7	707.87	1549.26	2.189	3
E4226		310.029	678.33	2.188	3
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...+2 564	5628.959	12298.63	2.185	3
E6419		1363.324	2955.49	2.168	4
E283	4115929 (AF118222) similar to the subtilase family of ...+2 386 3.€	3887.903	8406.49	2.162	3
E2477	4510339 (AC006921) putative ABC transporter protein [A...+1 621	6678.729	14414.78	2.158	3
E790	4734007 (AC007178) hypothetical protein [Arabidopsis t...+3 340	3800.266	8174.74	2.151	2
E3168	4468044 (X73587) catechol O-methyltransferase [Vanilla...+1 304	14742.91	31541.88	2.139	3
E2698	629602 probable imbibition protein - wild cabbage >em...+1 256 4	7844.019	16760.76	2.137	3
E2692	1708463 IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) I...+	2062.522	4351.95	2.11	1
E1869	2262177 (AC002329) hypothetical protein similar to T18...+3 337 1	1612.18	3393.53	2.105	4
E6635	2829898 (AC002311) Hypothetical protein [Arabidopsis t...+2 594	489.568	1024.92	2.094	1
E1962	BGL2	4653.505	9668.86	2.078	1
E4000		9621.166	19941.79	2.073	2
E2493		1270.596	2618.56	2.061	1
E1759	BGL2	7534.63	15510.94	2.059	3
E4000		8221.509	16922.77	2.058	2
E4015	jasmonate inducible protein	6181.416	12646.16	2.046	4
E4356	G993	2801.262	5728.43	2.045	3
E5608	4581500 (AL034352) putative oxalyl-CoA decarboxylase [...] +1 93	4182.265	8520.2	2.037	2
E6556		952.126	1937.51	2.035	1
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana] +2 25	1970.489	4000.44	2.03	3
E6342	3319340 (AF077407) contains similarity to E. coli cati...+1 187 5.9	1478.639	2998.26	2.028	2
E2533		1268.852	2560.21	2.018	1
E5388	3281849 (AL031004) methyltransferase - like protein [A...+3 460 2	2819.618	5678.53	2.014	3
E4000	BGL2	8079.555	16254.56	2.012	1
E1918		8752.048	17603.95	2.011	3
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba...+3 178	8542.279	17137.85	2.006	3
E5868	2062157 (AC001645) jasmonate inducible protein isolog ...+3 886	2441.033	4890.12	2.003	1
E5232	1620371 (Y08782) peroxidase ATP23a [Arabidopsis thaliana] +1 7C	2499.636	4996.33	1.999	4
E6353		1493.74	2984.13	1.998	4
E5182	2062161 (AC001645) jasmonate inducible protein isolog ...+1 687	6163.866	12316.41	1.998	4
E2153		3758.09	7494.53	1.994	2
E4857	G22	538.358	1073.05	1.993	4

E5229	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	182	2.0	2642.593	5267.75	1.993	7	2	2	19
E4407	G353				1156.283	2298.5	1.988				
E5665	1531760 (X97075) proline oxidase [Arabidopsis thaliana]	+1	265	;	2837.362	5636.47	1.987	4	2	2	2
E5558	1403134 (X98453) peroxidase [Arabidopsis thaliana]	+3	485	1.	2296.018	3991.01	1.985	4	1	1	2
E5223	2578440 (X67425) pectinesterase [Pisum sativum]	+1	147	2.	5154.649	4536.75	1.976	4	4	4	6
E2444	G25				10141.33	10141.33	1.967	4	3	3	12
E4215	E6617	2062158 (AC001645) jasmonate inducible protein isolog ... +1	573		526.179	1034.51	1.966	1	4	4	22
E2449	3152575 (AC002986) Similar to cytochrome P450tyr gbjU3... +2	18			6129.129	12032.62	1.963	1	2	2	5
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR				3490.09	3490.09	1.961	1	1	1	7
E5556	E5433	1888.928			3563.413	6981.46	1.959	2	1	1	1
E6453	E6453	1888.928			3664.71	1.94	1.94	4	4	1	2
E5376	2213583 (AC000348) T7N9.3 [Arabidopsis thaliana]	+2	138	4	893.096	1730.51	1.938	2	2	2	5
E2259	4388826 (AC006528) hypothetical protein [Arabidopsis t... +1	313	;	3509.178	6795.64	1.937	1	1	1	1	2
E5640	2827524 (AL021633) predicted protein [Arabidopsis thal... +2	100	;	5777.452	11192.55	1.937	1	1	1	1	12
E4345	G867	1826.633			3536.2	1.936	2	1	1	1	2
E5710	2829927 (AC002291) Unknown protein [Arabidopsis thaliana] +2	82		4834.983	9357.07	1.935	3	1	1	1	20
E6344	3319340 (AF077407) contains similarity to E. coli cati... +3	172	2.0	2456.18	4727.44	1.925	4	2	2	2	2
E4000	BGL2	1316.844			2531.77	1.923	2	3	3	3	4
E6580	4455239 (AL035523) abscisic acid-induced-like protein ... +1	160	5	9295.127	17876.85	1.923	1	1	1	1	1
E717	3860163 (AF098962) disease resistance protein RPP1-WsA... +2	1		2055.992	3943.99	1.918	3	3	3	3	6
E6357	1742959 (Z71450) CLC-d chloride channel protein [Arabi... +2	251		8219.533	15756.45	1.917	2	1	1	1	10
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana]	+2	727	,	2018.472	3853.98	1.909	3	1	1	4
E4015	jasmonate inducible protein			13445.38	25668.72	1.909	3	1	1	1	18
E6475	3080373 (AL022580) putative protein [Arabidopsis thali... +3	398	1.	5557.416	10581.41	1.904	3	3	3	1	1
E6646	3164144 (D78607) cytochrome P450 monooxygenase [Arabid... +1	1698.138		1587.869	3009.22	1.895	4	2	2	2	4
E6933	3522935 (AC004411) putative alcohol dehydrogenase [Ara... +1	58:	2374.517	3217.31	1.895	1	1	1	1	1	6
E5465	4587529 (AC007060) Strong similarity to F19I3.2 gj303... +1	338	6	1079.61	4499.76	1.895	1	1	2	2	7
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t... +1	125		9302.381	17619.53	1.894	3	3	3	3	8
E2950	E2396	2629.198			17619.53	4977.57	1.893	3	4	4	13
E6710	1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go... +2	231	5	5303.551	10014.84	1.888	4	1	1	1	12
E6975	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+2	694	2.	1556.397	2935.39	1.886	1	1	1	7
E3160	2286069 (U72155) beta-glucosidase [Arabidopsis thaliana]	+1	777		19083.13	35984.08	1.886	1	3	3	14
E800	E4224	2004.438			3948.593	7437.16	1.884	2	4	4	10
		956.68			956.68	1799.49	1.881	2	2	2	22

Summary of Overexpressor G28, Family AP2

Mendel Biotechnology, Inc.

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G28 corresponds to *AtERF1* (GenBank accession number AB008103) (Fujimoto et al., 2000). G28 appears as gene AT4g17500 in the annotated sequence of Arabidopsis chromosome 4 (AL161546.2).

AtERF1 has been shown to have GCC-box binding activity [some defense-related genes that are induced by ethylene were found to contain a short cis-acting element known as the GCC-box: AGCCGCC (Ohme-Takagi and Shinshi, 1990)]. Using transient assays in Arabidopsis leaves, *AtERF1* was found to be able to act as a GCC-box sequence specific transactivator (Fujimoto et al., 2000).

AtERF1 expression has been described to be induced by ethylene (two- to three-fold increase in *AtERF1* transcript levels 12 h after ethylene treatment) (Fujimoto et al., 2000). In the *ein2* mutant, the expression of *AtERF1* was not induced by ethylene, suggesting that the ethylene induction of *AtERF1* is regulated under the ethylene signaling pathway (Fujimoto et al., 2000). *AtERF1* expression was also induced by wounding, but not by other abiotic stresses (such as cold, salinity, or drought) (Fujimoto et al., 2000).

It has been suggested that AtERFs, in general, may act as transcription factors for stress-responsive genes, and that the GCC-box may act as a cis-regulatory element for biotic and abiotic stress signal transduction in addition to its role as an ethylene responsive element (ERE) (Fujimoto et al., 2000), but there is no data available on the physiological functions of *AtERF1*.

Mendel Discoveries

The function of G28 was analyzed at Mendel using transgenic plants in which this gene was expressed under the control of the 35S promoter. G28 overexpressing lines are more tolerant to infection with a moderate dose of the fungal pathogen *Erysiphe orontii*. G28 overexpression does not seem to have detrimental effects on plant growth or vigor, since plants from most of the lines are morphologically wild-type. In addition, no difference was detected between those lines and the corresponding wild-type controls in all the biochemical assays that were performed.

G28 is ubiquitously expressed, and it is not significantly induced under any of the conditions tested (which did not include ethylene treatment).

Closely Related Genes from Other Species

The non-Arabidopsis gene most closely related to G28 is an AP2-related transcription factor gene from *Mesembryanthemum crystallinum* (GenBank accession number AF245119), for which no functional information is available.

Conversely, G28 is the Arabidopsis gene most closely related to *Mesembryanthemum* AF245119. Similarity extends between the conserved AP2 domain, which is nearly 100% identical between these two proteins, raising the possibility that the two genes are orthologs.

Utilities

G28 transgenic plants have an altered response to the fungal pathogen *Erysiphe orontii*, in that those plants are more tolerant to that pathogen. Therefore, G28 could be used to manipulate the defense response in order to generate

pathogen-resistant plants.

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Keywords

Disease, Erysiphe

Knockout Status

KO DNA insertion not identified

Plasmid ID P174

Cloning Vector pMEN20

Cloning Site NA

Source DNA L22P3E10

Bacterial Strain DH5a

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Patent Information

Disease-Induced Polynucleotides, 3/22/00

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